

00431PHRM293.ST25
SEQUENCE LISTING

<110> Vogeli, Gabriel
Huff, Rita
Sejlitz, Torsten
Lind, Peter
Slightom, Jerry
Schellin, Kathleen
Bannigan, Chris
Ruff, Valerie
Kaytes, Paul
Wood, Linda
Parodi, Luis
Hiebsch, Ronald

<120> Novel G Protein Coupled Receptors

<130> 00431PHRM293

<150> 60/165,838

<151> 1999-11-16

<150> 60/198,568

<151> 2000-04-20

<150> 60/166,071

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<151> 2000-05-02

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<160> 190

<170> PatentIn version 3.0

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<211> 1182

<212> DNA

<213> H.Sapiens

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ttctctgccc ttaccgtctt agccatcaaa ctctgagctg gagatagtga cgatgtgaca      180
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ggtgagcacc ttcttctact ctagggccat gtggtagagc tgcagtcgca cctccttctg      300
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ccgttccagc actaggtaga ggtgacactc ctggcaggcc acctgcacaa tgccagtgat      420
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tttgaagtcg ctgggagtcc gtggggatcg ataacctcca gccatggctc ctgcatgttc      540
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ggccacgaac ccactcatga tcttcaagta gcggaagggc tgcttgatgg caaggtacct      840
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catccgcagg ctgcacaggg tcttctgtgt gggccgagaa gggtggaga gctggtctgt      960
gagtaggcca gagatggcca caccaatcaa ggtgtcagcc acagccagat tcaaggtgaa     1020
gcagagactg acaccatcat tcttgtggat caacagcagc acagccacag ccactagtgt     1080
gttagtagca atgatgaggg aggccaggac agcaaggatc actccaaatg agaaagatga     1140
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20          25          30
Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
35          40          45
Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
50          55          60
Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
65          70          75          80
Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
85          90          95
Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
100         105         110
Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
115         120         125
Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
130         135         140
Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
145         150         155         160
Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
165         170         175
Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
180         185         190
Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
195         200         205
Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
210         215         220
Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
225         230         235         240
Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
245         250         255
Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
260         265         270
Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu

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275

280

285

Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
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Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu
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 acaggacgcg aaggcgctgc tgtagccaag ccacgagcag ccaagtgcag cgctgagaa 240
 ggccagcgac tgtccccagg cacagcccag cagcaggccg gcatagcgcg gtgcgaggcg 300
 tccggcgtag cgcagtggga agccactgc cagccactgg tctgcgctca gcgcgccac 360
 gctcagcgcc gcgttggacg ccaggaaggt gtccaggaag ccaatgactt ggcatgcgcc 420
 gggcgccgac ggtgtccgcc cgcgcacac accgagcagc gtgaagggca tgtccagcgc 480
 cgccagcagc aggtggccca gagacagatt caccaggagg acgcctgagg ctcgagtgcg 540
 gagctcagcg ctgtaggcgc aacaaagcag caccagtgcg ttggatagca gcgccacggc 600
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<212> PRT

<213> H.Sapiens

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 20 25 30

Ala Tyr Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val
 35 40 45

Asn Leu Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe
 50 55 60

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Thr Leu Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala
65 70 75 80

Cys Gln Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala
85 90 95

Leu Ser Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe
100 105 110

Pro Leu Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu
115 120 125

Leu Gly Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu
130 135 140

Gly Cys Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu
145 150 155 160

Arg Leu Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala
165 170 175

Thr Leu His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu
180 185 190

Thr Ser Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met
195 200 205

Asp Thr Val Thr Met Lys Ala Leu Ala
210 215

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<212> DNA

<213> H.Sapiens

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tataacattg tcctcatcag ctatgatcga tacctgtcag tctcaaagtc tgtaagtcga 180

acacattaat ttatccccct tagaagatta tgtaaagtga ta 222

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<212> PRT

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Glu Trp Asp Phe Gly Lys Glu Ile Cys Val Phe Trp Leu Thr Thr Asp
20 25 30

Tyr Leu Leu Cys Thr Ala Ser Val Tyr Asn Ile Val Leu Ile Ser Tyr

35

40

45

Asp Arg Tyr Leu Ser Val Ser Asn Ala Val Ser Arg Thr His Phe Ile
 50 55 60

Pro Leu Arg Arg Leu Cys Lys Cys Ile
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 acgacggcgg cgccagcgct tggagctgag cgggtacagg atccccagga agcgctccac 180
 gctgatacag gtcattggtga ggatgctgga atacatgttt gcgtaaaagg ccacgggtcac 240
 cacgttgcaa agcagcaccc cgaataccca gtggtggcgg ttgcaatggt agtagatttg 300
 gaaaggcaac acgctggcca gcatcaggtc cgtgacgctc aggttgatca tgaagatgac 360
 cgacggggat ctggggcccca tgcgcgggca cagcaccac agagagaaga gggtgcccgg 420
 gatgctgacc gccgcacca gcgagtacac cacgggcagg gccaccgcga tcgccgggtt 480
 ccgcagcatc tgcagcgctc cgttgctc 507

<210> 8

<211> 169

<212> PRT

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Leu Pro Val Val Tyr Ser Leu Val Ala Ala Val Ser Ile Pro Gly Asn
 20 25 30

Leu Phe Ser Leu Trp Val Leu Cys Arg Arg Met Gly Pro Arg Ser Pro
 35 40 45

Ser Val Ile Phe Met Ile Asn Leu Ser Val Thr Asp Leu Met Leu Ala
 50 55 60

Ser Val Leu Pro Phe Gln Ile Tyr Tyr His Cys Asn Arg His His Trp
 65 70 75 80

Val Phe Gly Val Leu Cys Asn Leu Val Val Thr Val Ala Phe Tyr Ala
 85 90 95

Asn Met Tyr Ser Ser Ile Leu Thr Met Thr Cys Ile Ser Val Glu Arg

100

105

110

Phe Leu Gly Ile Leu Tyr Pro Leu Ser Ser Lys Arg Trp Arg Arg Arg
 115 120 125

Arg Tyr Ala Val Ala Ala Cys Ala Gly Thr Trp Leu Leu Leu Leu Thr
 130 135 140

Ala Leu Ser Pro Leu Ala Arg Thr Asp Leu Thr Tyr Pro Val His Ala
 145 150 155 160

Leu Gly Ile Ile Thr Cys Phe Asp Val
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<210> 9
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 gcacgggagg gaggcgtctt cgtggcactc actgcgtccg tgctgagcct cctgggcac 180
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 cgcacgctgg cgatggcagc cgcggcctgg 270

<210> 10
 <211> 90
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 Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu
 20 25 30
 Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val
 35 40 45
 Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Gly Ile Ala Leu Glu Arg
 50 55 60
 Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly
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 Arg Thr Leu Ala Met Ala Ala Ala Ala Trp
 85 90

<210> 11
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gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac      180
tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacagggcc      240
gggagcatcg tgttccttac ggtgggtggct gcggacaggt atttcaaagt ggtccacccc      300
caccacgcgg tgaacactat ctccaccggt gtggcggtctg gcatcgtctg caccctgtgg      360
gccctgggtca tcctgggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag      420
acggccgtct cctgtgagag cttcatcatg gagtcggcca atggctggca tgacatcatg      480
ttccagctgg agttctttat gcccctcggc atcatcttat tttgctcctt caagattggt      540
tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgaccggt      600
ttcatcatgg tggtggaat tgtgttcac acatgctacc tgcccagcgt gtctgctaga      660
ctctatttcc tctggacggt gccctcgagt gcctgcgac cctctgtcca tggggccctg      720
cacataaccc tcagcttcac ctacatgaac agcatgctgg atccccctgg gtattatttt      780
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<210> 12

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<212> PRT

<213> H.Sapiens

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Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Met Ile Cys Leu
35          40          45
Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His Trp Ala Phe Gly
50          55          60
Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala Met Asn Arg Ala
65          70          75          80
Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp Arg Tyr Phe Lys
85          90          95

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Val Val His Pro His His Ala Val Asn Thr Ile Ser Thr Arg Val Ala
100 105 110

Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile Leu Gly Thr Val
115 120 125

Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu Thr Ala Val Ser
130 135 140

Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met
145 150 155 160

Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser
165 170 175

Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln Leu Ala Arg Gln
180 185 190

Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val
195 200 205

Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu
210 215 220

Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu
225 230 235 240

His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu
245 250 255

Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu
260 265 270

Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His Ser Lys Thr Gln
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Arg Pro Glu Glu Met Pro Ile Ser
290 295

<210> 13

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<212> DNA

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tgcaagctgg tgcacttcct gttctatata aacctttacg gcagcatcct gctgctgacc 180

tgcattctctg tgcaccagtt cctaggtgtg tgccaccacac tgtgttcgct gccctaccgg 240

acccgcaggc atgcctggct gggcaccagc accacctggg ccctggtggt cctccagctg 300

ctgcccacac tggccttctc ccacacggac tacatcaatg gccagatgat ctggtatgac 360

atgaccagcc aagagaattt tgatcggtt tttgcctacg gcatagttct gacattgtct 420

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caagccagag gagaacctca tgaggacagg 510

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Arg Trp Pro Phe Gly Glu Leu Leu Cys Lys Leu Val His Phe Leu Phe
35 40 45
Tyr Ile Asn Leu Tyr Gly Ser Ile Leu Leu Leu Thr Cys Ile Ser Val
50 55 60
His Gln Phe Leu Gly Val Cys His Pro Leu Cys Ser Leu Pro Tyr Arg
65 70 75 80
Thr Arg Arg His Ala Trp Leu Gly Thr Ser Thr Thr Trp Ala Leu Val
85 90 95
Val Leu Gln Leu Leu Pro Thr Leu Ala Phe Ser His Thr Asp Tyr Ile
100 105 110
Asn Gly Gln Met Ile Trp Tyr Asp Met Thr Ser Gln Glu Asn Phe Asp
115 120 125
Arg Leu Phe Ala Tyr Gly Ile Val Leu Thr Leu Ser Gly Phe Leu Ser
130 135 140
Leu Leu Gly His Phe Gly Val Leu Phe Thr Asp Gly Gln Glu Pro Asp
145 150 155 160
Gln Ala Arg Gly Glu Pro His Glu Asp Arg
165 170

<210> 15
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<222> (431)..(461)
<223> n is any nucleotide

<400> 15
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ccaccagacg gagagtaggt ggccacaagc gacacccatg atcttaacag gcgcgacgaa 300
gcccgcgacg gcctcataga acgcgtacac ctgcacgtgc cagcgtgca ggagcgcgaa 360
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cacgaggtgg gccgaggcgc cccgcccgga tgctgcagc agctgcagga agcggcacgc 660
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cgtgcccccg cacgcgtaca ggtccgccag ggccagctgc accagcagga agtccatctt 780
gcgacgcttn nnnnnnnnnn nnnnnnnnnn nnnnnnnnac aggcggcaca gcaactgtgt 840
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<210> 16
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20          25          30

Xaa Xaa Xaa Lys Arg Arg Lys Met Asp Phe Leu Leu Val Gln Leu Ala
35          40          45

Leu Ala Asp Leu Tyr Ala Cys Gly Gly Thr Ala Leu Ser Gln Leu Ala
50          55          60

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Trp Glu Leu Leu Gly Glu Pro Arg Ala Ala Thr Gly Asp Leu Ala Cys
 65 70 75 80
 Arg Phe Leu Gln Leu Leu Gln Ala Ser Gly Arg Gly Ala Ser Ala His
 85 90 95
 Leu Val Val Leu Ile Ala Leu Glu Arg Arg Arg Ala Val Arg Leu Pro
 100 105 110
 His Gly Arg Pro Leu Pro Ala Arg Ala Leu Ala Ala Leu Gly Trp Leu
 115 120 125
 Leu Ala Leu Leu Leu Ala Arg Gly Ser Gly Phe Val Val Arg Tyr Xaa
 130 135 140
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Leu Gln Pro Gly
 145 150 155 160
 Ala Pro Leu Ser Ala Arg Ala Trp Pro Gly Met Arg Arg Cys His Trp
 165 170 175
 Ile Phe Ala Leu Leu Gln Arg Trp His Val Gln Val Tyr Ala Phe Tyr
 180 185 190
 Glu Ala Val Ala Gly Phe Val Ala Pro Val Lys Ile Met Gly Val Ala
 195 200 205
 Cys Gly His Leu Leu Ser Val Trp Trp Arg His Arg Leu Lys Ala Pro
 210 215 220
 Ala Gly Ala Ala Ala Trp Ser Ala Ser Pro Gly Gly Ala Arg Ala Pro
 225 230 235 240
 Ser Ala Met Pro Arg Ala Lys Val Gln Ser Leu Lys Met Ser Gln Leu
 245 250 255
 Leu Gly Leu Leu Phe Val Gly Cys Glu Leu Pro Phe Ala Asp Arg Leu
 260 265 270
 Glu Ala Ala Trp Ser Ser Gly Pro Ala Gly Glu Trp Glu Gly Glu Ala
 275 280 285
 Leu Ser Ala Cys Cys Ala Trp Trp
 290 295

<210> 17

<211> 801

<212> DNA

<213> H.Sapiens

<400> 17

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ggggaggagg tagaatagga aggaggtgac ctggatgatg aaattgtaga tccacatggg 180

cttgatgacc gtacaggtgg ccgaacctgg gaccagggac ccattgggga agtagtgga 240

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gccgaggatc ctgagggccc ggcgccgggt gctctgcagt ttggcgcgga acgggtgtag      360
gatggccacg tagcgctcca cgctgacggt ggtgatgctg aggatggagg cgaagcacac      420
ggtctcaaag agggccgtct tgaagtagca gcccacgggc ccgaacaaga aagggtagtt      480
gcgccacatc tcatagacct ccaggggcat tccaaggagc aggaccagga ggtagagac      540
cgccaggctg aagaggtagt agttgggtgg cgtcttcata gcctgggtgct gcagaatcac      600
caggcacacc aggacattgc caatgacccc caccacaaaa attggcacat acaccacaga      660
cacggggagg aagaagtggc tgcgccgagg tccgcagagg aaggccagat actcctcggt      720
gctgttcagg tgtttctgga atggatcttc tagtttctgc tggtagatcc aggaagcatt      780
ctgaagtttt tccatccctg a                                              801

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<210> 18
<211> 249
<212> PRT
<213> H.Sapiens

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<400> 18

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Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
20          25          30
Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
35          40          45
Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu
50          55          60
Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Asn Thr
65          70          75          80
Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu
85          90          95
Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu
100          105          110
Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val
115          120          125
Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr
130          135          140
Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg
145          150          155          160

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Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe
 165 170 175
 Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro
 180 185 190
 Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro
 195 200 205
 Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr
 210 215 220
 Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu
 225 230 235 240
 Arg Val Ser Ile Ala Gly Val Ala Gly
 245

<210> 19
 <211> 222
 <212> DNA
 <213> H.Sapiens

<400> 19
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 attgtctatg catttatgaa tgaaaacttc aaaaaaatg ttttgtctgc agtttgttat 120
 tgcatagtaa ataaaacctt ctctccagca caaaggcatg gaaattcagg aattacaatg 180
 atgcggaaga aagcaaagtt ttccctcaga gagaatccag tg 222

<210> 20
 <211> 73
 <212> PRT
 <213> H.Sapiens

<400> 20

Ile Lys Met Ile Phe Ala Ile Val Gln Ile Ile Gly Phe Ser Asn Ser
 1 5 10 15
 Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu Asn Phe Lys Lys
 20 25 30
 Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn Lys Thr Phe Ser
 35 40 45
 Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met Met Arg Lys Lys
 50 55 60
 Ala Lys Phe Ser Leu Arg Glu Asn Pro
 65 70

<210> 21
 <211> 447
 <212> DNA
 <213> H.Sapiens

1 . 5 10 15

Leu Arg Leu Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser
 20 25 30

Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg
 35 40 45

Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg
 50 55 60

Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser
 65 70 75 80

Pro Gly

<210> 27
 <211> 420
 <212> DNA
 <213> H.Sapiens

<220>
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 <222> (81)..(106)
 <223> n is any nucleic acid

<400> 27
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 cgcgatgcgg gcgtacatga ccacgatgag cgccagcggc gccaggtaga tgtgcgagaa 180
 gagcacagtg gtgtagaccc tgcgcatgcc cttctcgggc caggcctccc agcaggagta 240
 gagagggtag gagcggttgc gggcgtccac catgaagtgg tgctcctcac gggtgacggt 300
 cagcgtgacg gccgagggac acatgatgag cagcgccagg gcccagatga cggcgatggt 360
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<210> 28
 <211> 139
 <212> PRT
 <213> H.Sapiens

<220>
 <221> UNSURE
 <222> (104)..(113)
 <223> Xaa is Unknown

<400> 28

Phe Arg Cys Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys
 1 5 10 15

Ala Leu Val Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met
20 25 30

Cys Pro Ser Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe
35 40 45

Met Val Asp Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu
50 55 60

Ala Trp Pro Glu Lys Gly Met Arg Arg Val Tyr Thr Thr Val Leu Phe
65 70 75 80

Ser His Ile Tyr Leu Ala Pro Leu Ala Leu Ile Val Val Met Tyr Ala
85 90 95

Arg Ile Ala Arg Lys Leu Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
100 105 110

Xaa Glu Ala Ala Asp Pro Arg Ala Ser Arg Arg Arg Ala Arg Val Val
115 120 125

His Met Leu Val Met Val Ala Leu Phe Phe Thr
130 135

<210> 29
<211> 318
<212> DNA
<213> H.Sapiens

<400> 29
gcagggggcg tgagtcctca ggcacttctt gaggtccttg ttgagcagga agcagacaat 60
tgggttgacg gcagcctggg cgaagctcat ccaaacagca gtggccaggt agcgggtgggg 120
cacagcacag gctttcacaa aactcgcga gtagcaggcc acgatgtagg gtgaccagag 180
gagcagaaaag agcagtgtga tcgcgtagaa catgçggccc agctgctttt cacccttgac 240
ctcgccatg cccagtagcc gccggctggc tgcattccca ttctgccgga taccagcag 300
ggttggtggc atgggccc 318

<210> 30
<211> 106
<212> PRT
<213> H.Sapiens

<400> 30

Gly Pro Met Pro Pro Thr Leu Leu Gly Ile Arg Gln Asn Gly His Ala
1 5 10 15

Ala Ser Arg Arg Leu Leu Gly Met Asp Glu Val Lys Gly Glu Lys Gln
20 25 30

Leu Gly Arg Met Phe Tyr Ala Ile Thr Leu Leu Phe Leu Leu Leu Trp
35 40 45

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Ser Pro Tyr Ile Val Ala Cys Tyr Trp Arg Val Phe Val Lys Ala Cys
50 55 60

Ala Val Pro His Arg Tyr Leu Ala Thr Ala Val Trp Met Ser Phe Ala
65 70 75 80

Gln Ala Ala Val Asn Pro Ile Val Cys Phe Leu Leu Asn Lys Asp Leu
85 90 95

Lys Lys Cys Leu Arg Thr His Ala Pro Cys
100 105

<210> 31
<211> 354
<212> DNA
<213> H.Sapiens

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cattgtgaaa gcccttcggt tgggtgtattg ccacttcatt ttaaaaggat gcacaagtcc 120
ctggtgcctt tccacagcaa tgcaggtcat agtgaggatt tctgtcacao cagcggtaga 180
ctggacaaat ggcaccatct tgcaaatgaa agcacctgca gtaaggaaat aggataaatc 240
atacatcaaa acaaaaagaa taaaggtttc atctgtgtct ttgtaattat cactatcagt 300
ccattctgag cctctgccaa aaagtttgat aattgtaatt actctgtaga caca 354

<210> 32
<211> 117
<212> PRT
<213> H.Sapiens

<400> 32

Val Tyr Arg Val Ile Thr Ile Ile Lys Leu Phe Gly Arg Gly Ser Glu
1 5 10 15

Trp Thr Asp Ser Asp Asn Tyr Lys Asp Thr Asp Glu Thr Phe Ile Leu
20 25 30

Phe Val Leu Met Tyr Asp Leu Ser Tyr Phe Leu Thr Ala Gly Ala Phe
35 40 45

Ile Cys Lys Met Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu
50 55 60

Ile Leu Thr Met Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val
65 70 75 80

His Pro Phe Lys Met Lys Trp Gln Tyr Thr Asn Arg Arg Ala Phe Thr
85 90 95

Met Leu Gly Glu Ala Thr Gly Cys Ala Asn Gly Ser Val Asn Asp Ile
100 105 110

Leu His Tyr Arg Ile
115

<210> 33
<211> 621
<212> DNA
<213> H.Sapiens

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agtgttgatc atgctgttgc tcatggcgat gcactcgacg atgtagaagg cagtgaggta 120
gtgcttctcc ttcacaaaca cgggtgggaa gaagtcgagc acgatgggtga agccgtagaa 180
gggcgcccag catagcacgt aggcgggtgag gatgcacatg agcaccagga ccgtcttcct 240
gcggcagcgc agcctcttgc ggatctgctc tgtctggaat ccagggaccg ccttgaacca 300
gagctcccgaggatcctgg catagcacag ggtcatgggtg accacggggc ccacgaattc 360
tatgccaaag ataaagagga agtaggactt gtagtagagc tgctggtcca caggccagat 420
ctggccgcag aagatctttt cctgggtctt gacaatgacg aggaccgtct cgggtggtgaa 480
gtaggcggaa gggatggcga tcaggatgga caccgtccac accaaggcaa tcaggccagt 540
ggctgtttgg cacttcattc gtggtctcag cggatggaca atagccagat acctagggca 600
agaacacaag tggaggcagc c 621

<210> 34
<211> 207
<212> PRT
<213> H.Sapiens

<400> 34
Gly Cys Leu His Leu Cys Ser Cys Pro Arg Tyr Leu Ala Ile Val His
1 5 10 15
Pro Leu Arg Pro Arg Met Lys Cys Gln Thr Ala Thr Gly Leu Ile Ala
20 25 30
Leu Val Trp Thr Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe
35 40 45
Thr Thr Glu Thr Val Leu Val Ile Val Lys Ser Gln Glu Lys Ile Phe
50 55 60
Cys Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr
65 70 75 80
Phe Leu Phe Ile Phe Gly Ile Glu Phe Val Gly Pro Val Val Thr Met
85 90 95
Thr Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Val

100

105

110

Pro Gly Phe Gln Thr Glu Gln Ile Arg Lys Arg Leu Arg Cys Arg Arg
 115 120 125

Lys Thr Val Leu Val Leu Met Cys Ile Leu Thr Ala Tyr Val Leu Cys
 130 135 140

Trp Ala Pro Phe Tyr Gly Phe Thr Ile Val Arg Asp Phe Phe Pro Thr
 145 150 155 160

Val Phe Val Lys Glu Lys His Tyr Leu Thr Ala Phe Tyr Ile Val Glu
 165 170 175

Cys Ile Ala Met Ser Asn Ser Met Ile Asn Thr Leu Cys Phe Val Thr
 180 185 190

Val Lys Asn Asp Thr Val Lys Tyr Phe Lys Lys Ile Met Leu Leu
 195 200 205

<210> 35
 <211> 483
 <212> DNA
 <213> H.Sapiens

<400> 35
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 taagaagcca caaaaacttcc cttccagggt gttcagcagc agggacaggg cccagggcag 120
 ggcacacatg acagttgaca ggtttcttgg gcagcagcag cagtaccaga taggccgcag 180
 gacagacagg cagcactcag tactgatggc actcagcatg ctcaggccta caaggtaggc 240
 aaaggctcatc acgctggtga agaagctagg gaaattgatg gagatggaac agaagaagtt 300
 actgaggtac accaggcaat ttataatctg gaagcagagg aagaggaagt cggccccggc 360
 caggctgagg acgtagacag agaaggcgtt cctgcgcagc cggaagccca ggagccagag 420
 cacaaacccg tttcctacga gcccagaccag ggcaatgaaa aggatcagga agaccgggat 480
 cag 483

<210> 36
 <211> 161
 <212> PRT
 <213> H.Sapiens

<400> 36

Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala Leu Val Gly Leu Val
 1 5 10 15

Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn
 20 25 30

Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe

35

40

45

Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe
 50 55 60
 Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Ser Val Met Thr
 65 70 75 80
 Phe Ala Tyr Leu Val Gly Leu Ser Met Leu Ser Ala Ile Ser Thr Glu
 85 90 95
 Cys Cys Leu Ser Val Leu Arg Pro Ile Trp Tyr Cys Cys Cys Cys Pro
 100 105 110
 Arg Asn Leu Ser Thr Val Met Cys Ala Leu Pro Trp Ala Leu Ser Leu
 115 120 125
 Leu Leu Asn Thr Leu Glu Gly Lys Phe Cys Gly Phe Leu Val Ser Asn
 130 135 140
 Gly Asp Tyr Gly Trp Cys Trp Thr Phe Asp Phe Ile Thr Ala Val Trp
 145 150 155 160

Leu

<210> 37
 <211> 330
 <212> DNA
 <213> H.Sapiens

<400> 37
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 atcctttgct tgtccgttga ggtcctagtc tggagccaag tgacaaagac agagatcacc 120
 tatttacgcc atgtgtgcat tgtaacatt gcagccactt tgctgatggc agatgtgtgg 180
 ttcatgtgg cttcctttct tagtggccca ataacacacc acaagggatg tgtggcagcc 240
 acattttttg gtcatttctt ttacctttct gtatttttct ggatgcttgc caaggcactc 300
 cttatcctct atggaatcat gattgttttc 330

<210> 38
 <211> 110
 <212> PRT
 <213> H.Sapiens

<400> 38

Glu Ser Leu Ile Leu Thr Tyr Ile Thr Tyr Val Gly Leu Gly Ile Ser
 1 5 10 15
 Ile Cys Ser Leu Ile Leu Cys Leu Ser Val Glu Val Leu Val Trp Ser
 20 25 30
 Gln Val Thr Lys Thr Glu Ile Thr Tyr Leu Arg His Val Cys Ile Val

35

40

45

Asn Ile Ala Ala Thr Leu Leu Met Ala Asp Val Trp Phe Ile Val Ala
50 55 60

Ser Phe Leu Ser Gly Pro Ile Thr His His Lys Gly Cys Val Ala Ala
65 70 75 80

Thr Phe Phe Gly His Phe Phe Tyr Leu Ser Val Phe Phe Trp Met Leu
85 90 95

Ala Lys Ala Leu Leu Ile Leu Tyr Gly Ile Met Ile Val Phe
100 105 110

<210> 39

<211> 628

<212> DNA

<213> H.Sapiens

<400> 39

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ctttaaatga ggacagtaaa tcccatacgg caggggtggtg gggagaatca gagatgatac 180
agctggtgat cacatctggt ttgtgttccc aggggcacca gactagggtt tctgagcatg 240
gatccaaccg tcccagtctt cggtacaaaa ctgacaccaa tcaacggacg tgaggagact 300
ccttgctaca atcagaccct gagcttcacg gtgctgacgt gcatcatttc ccttgctcgga 360
ctgacaggaa acgcggtagt gctctggctc ctgggctacc gcatgcgag gaacgctgtc 420
tccatctaca tcctcaacct ggccgcagca gacttcctct tcctcagctt ccagattata 480
cgttcgccat tacgcctcat caatatcagc catctcatcc gcaaaatcct cgtttctgtg 540
atgacctttc cctactttac aggcctgagt atgctgagcg ccatcagcac cgagcgctgc 600
ctgtctgttc tgtggcccat ctggtacc 628

<210> 40

<211> 205

<212> PRT

<213> H.Sapiens

<400> 40

Leu Cys Gly Ser Arg Glu Met Ser Gly Phe Arg Val Asn Lys Asn Trp
1 5 10 15

Ile Ser Asn Trp Ile Gly Pro Pro Pro Leu Val Ser Asp Leu Leu Ser
20 25 30

Ala Ser Leu Cys Phe Ser Leu Leu Met Arg Thr Val Asn Pro Ile Arg
35 40 45

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Gln Gly Gly Gly Glu Asn Gln Arg Tyr Ser Trp Ser His Leu Val Cys
50 55 60

Val Pro Arg Gly Thr Arg Leu Gly Phe Leu Ser Met Asp Pro Thr Val
65 70 75 80

Pro Val Phe Gly Thr Lys Leu Thr Pro Ile Asn Gly Arg Glu Glu Thr
85 90 95

Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val Leu Thr Cys Ile Ile
100 105 110

Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly
115 120 125

Tyr Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Ala
130 135 140

Ala Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile Ile Arg Ser Pro Leu
145 150 155 160

Arg Leu Ile Asn Ile Ser His Leu Ile Arg Lys Ile Leu Val Ser Val
165 170 175

Met Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met Leu Ser Ala Ile Ser
180 185 190

Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
195 200 205

<210> 41
<211> 319
<212> DNA
<213> H.Sapiens

<400> 41
acagaaagca aggccaccag gaccttaggc atagtcacatg gagtggttgt gttgtgctgg 60
ctgcccttct ttgtcttgac gatcacagat cctttcatta attttacaac ctttgaagat 120
ctgtacaatg tcttcctcctg gctaggctat ttcaactctg ctttcaatcc cattttatat 180
ggcatgcttt atccttggtt tcgcaaggca ttgaggatga ttgtcacagg catgatcttc 240
caccctgact cttccaccct aagcctgttt tctgcccacg cttaggctgt gttcatcatt 300
caataggact cttttctgg 319

<210> 42
<211> 103
<212> PRT
<213> H.Sapiens

<400> 42

Thr Glu Ser Lys Ala Thr Arg Thr Leu Gly Ile Val Met Gly Val Phe
1 5 10 15

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Val Leu Cys Trp Leu Pro Phe Phe Val Leu Thr Ile Thr Asp Pro Phe
 20 25 30
 Ile Asn Phe Thr Thr Leu Glu Asp Leu Tyr Asn Val Phe Leu Trp Leu
 35 40 45
 Gly Tyr Phe Asn Ser Ala Phe Asn Pro Ile Leu Tyr Gly Met Leu Tyr
 50 55 60
 Pro Trp Phe Arg Lys Ala Leu Arg Met Ile Val Thr Gly Met Ile Phe
 65 70 75 80
 His Pro Asp Ser Ser Thr Leu Ser Leu Phe Ser Ala His Ala Ala Val
 85 90 95
 Phe Ile Ile Gln Asp Ser Phe
 100

<210> 43
 <211> 515
 <212> DNA
 <213> H.Sapiens

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 aacaaatgct ttagaacaac tggtgaatgt attgtcctac aacttggcat atgatcatgc 180
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 aggtctctac agtaatgttt ttaatctgtc tctacttctt cagaaaataa attagttgtt 300
 gacgaatcag tccttaagac cttgccgctt acaataagtt ttattgcctt cccaaacccat 360
 tggtaaaaga aagcataaat caaggggttc atagctgaat tataataaac acaccaaact 420
 aaaatctcat aaacataagg aggagttata aaattcatat aagcatcaat cactgcatca 480
 acgagggtatg gtagccaaga gacaagaaat gctgc 515

<210> 44
 <211> 148
 <212> PRT
 <213> H.Sapiens

<400> 44

Leu His Gln Arg Gly Met Val Ala Lys Arg Gln Glu Met Leu Ala Ala
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 20 25 30
 Tyr Met Asn Phe Ile Thr Pro Pro Tyr Val Tyr Glu Ile Leu Val Trp
 35 40 45

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Cys Val Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Phe Phe
50 55 60

Tyr Gln Trp Phe Gly Lys Ala Ile Lys Leu Ile Val Ser Gly Lys Val
65 70 75 80

Leu Arg Thr Asp Ser Ser Thr Thr Asn Leu Phe Ser Glu Glu Val Glu
85 90 95

Thr Asp Lys His Tyr Cys Arg Asp Leu Lys Thr Asn Leu Lys Leu Arg
100 105 110

Ser Thr Ala Lys Ile Asn Thr Trp Thr Arg Gly Lys His Asp His Met
115 120 125

Pro Ser Cys Arg Thr Ile His Ser Thr Val Val Leu Lys His Leu Leu
130 135 140

Ser Ser Cys Ile
145

<210> 45
<211> 726
<212> DNA
<213> H.Sapiens

<400> 45
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gcgtttggaa acttactggt catgattgct atccttcact tctaacaact gcacacacct 120
acaaactttc tgattgcgtc gctggcctgt gctgacttct tgggtgggagt cactgtgatg 180
cccttcagca cagtgaggtc tgtggagagc tgttggtact ttggggacag ttactgtaaa 240
ttccatacat gttttgacac atctttctgt tttgcttctt tatttcattt atgctgtatc 300
tctgttgata gatacattgc tgttactgat cctctgacct atccaaccaa gtttactgtg 360
tcagtttcag ggatatgcat tgttctttcc tggttctttt ctgtcacata cagcttttcg 420
atcttttaca cgggagccaa cgaagaagga attgaggaat tagtagttgc tctaacctgt 480
gtaggaggct gccaggctcc actgaatcaa aactgggtcc tactttgttt tcttctattc 540
tttataacca atgtcgccat ggtgtttata tacagtaaga tatttttggt ggccaagcat 600
caggctagga agatagaaaag tacagccagc caagctcagt ccttctcaga gagttacaag 660
gaaagagtag caaaaagaga gagaaaggct gccaaaacct tgggaattgc tatggcagca 720
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<210> 46
<211> 241
<212> PRT
<213> H.Sapiens

<400> 46

Leu Glu Arg Gly Pro Arg Ser Ile Leu Tyr Ala Val Leu Gly Phe Gly
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 Ala Val Leu Ala Ala Phe Gly Asn Leu Leu Val Met Ile Ala Ile Leu
 20 25 30
 His Phe Gln Leu His Thr Pro Thr Asn Phe Leu Ile Ala Ser Leu Ala
 35 40 45
 Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Thr Val
 50 55 60
 Arg Ser Val Glu Ser Cys Trp Tyr Phe Gly Asp Ser Tyr Cys Lys Phe
 65 70 75 80
 His Thr Cys Phe Asp Thr Ser Phe Cys Phe Ala Ser Leu Phe His Leu
 85 90 95
 Cys Cys Ile Ser Val Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Thr
 100 105 110
 Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Val Leu
 115 120 125
 Ser Trp Phe Phe Ser Val Thr Tyr Ser Phe Ser Ile Phe Tyr Thr Gly
 130 135 140
 Ala Asn Glu Glu Gly Ile Glu Glu Leu Val Val Ala Leu Thr Cys Val
 145 150 155 160
 Gly Gly Cys Gln Ala Pro Leu Asn Gln Asn Trp Val Leu Leu Cys Phe
 165 170 175
 Leu Leu Phe Phe Ile Pro Asn Val Ala Met Val Phe Ile Tyr Ser Lys
 180 185 190
 Ile Phe Leu Val Ala Lys His Gln Ala Arg Lys Ile Glu Ser Thr Ala
 195 200 205
 Ser Gln Ala Gln Ser Phe Ser Glu Ser Tyr Lys Glu Arg Val Ala Lys
 210 215 220
 Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Ile Ala Met Ala Ala Phe
 225 230 235 240
 Leu

<210> 47

<211> 660

<212> DNA

<213> H.Sapiens

<400> 47

aaccaggtgg ccttactcct aagaccctg gccttgctta tggcctttat caacagctgt 60

ctcaatccag ttctctatgt cttcattggg catgacttct gggagcactt gctccactcc 120

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ctgctagctg ccttagaacg ggcacttagc gaggagccag atagtgcctg aatcccagct 180
cccaggcaga tgagtccttt ataacatgac ccaatttcct actccatttt cccaccactc 240
aatcctcttc ccaaacagct ctaccataat ccaacatcca acagaattta agagaataaa 300
ccacaacttt taagttagct ctatgtgcta ggtcatgttt tagaatacaa ccttaagtgc 360
ctggaagatg gaggcaagaa acaaacaagg tctcattctt tagaggaaga cagttcacca 420
agactcaaac agaaaaaaag atagttatct tgtgacaaaa caagtcataa aattgggtca 480
ggacctgcag caatgacttt atgctagaat ccagagcact agcaggaaaac tgcttaaatt 540
ttacttaatc aaagtcaagt ttggacatac atgtcaggta aaacctagca gagatgagct 600
accttgattt taaaacttca agggatagct caatgtcatc aagatccttt tgatgacttg 660

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<210> 48
<211> 211
<212> PRT
<213> H.Sapiens

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<400> 48

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Ile Asn Ser Cys Leu Asn Pro Val Leu Tyr Val Phe Ile Gly His Asp
20          25          30
Phe Trp Glu His Leu Leu His Ser Leu Leu Ala Ala Leu Glu Arg Ala
35          40          45
Leu Ser Glu Glu Pro Asp Ser Ala Ile Pro Ala Pro Arg Gln Met Ser
50          55          60
Pro Leu His Asp Pro Ile Ser Tyr Ser Ile Phe Pro Pro Leu Asn Pro
65          70          75          80
Leu Pro Lys Gln Leu Tyr His Asn Pro Thr Ser Asn Arg Ile Glu Asn
85          90          95
Lys Pro Gln Leu Leu Ser Glu Leu Tyr Val Leu Gly His Val Leu Glu
100         105         110
Tyr Asn Leu Lys Cys Leu Glu Asp Gly Gly Lys Lys Gln Thr Arg Ser
115         120         125
His Ser Leu Glu Glu Asp Ser Ser Pro Arg Leu Lys Gln Lys Lys Arg
130         135         140
Leu Ser Cys Asp Lys Thr Ser His Lys Ile Gly Ser Gly Pro Ala Ala
145         150         155         160
Met Thr Leu Cys Asn Pro Glu His Gln Glu Thr Ala Ile Leu Leu Asn
165         170         175

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Gln Ser Gln Val Trp Thr Tyr Met Ser Gly Lys Thr Gln Arg Ala Thr
 180 185 190

Leu Ile Leu Lys Leu Gln Gly Ile Ala Gln Cys His Gln Asp Pro Phe
 195 200 205

Asp Asp Leu
 210

<210> 49
 <211> 465
 <212> DNA
 <213> H.Sapiens

<400> 49
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 agcggaggcg cgcggtgggc ctggccgcgg tgggtcttgc ggcctttgtc acctgcttcg 120
 cccccaacaa cttcgtgctc ctggcgcaca tcgtgagccg cctgttctac ggcaagagct 180
 actaccacgt gtacaagctc acgctgtgtc tcagctgcct caacaactgt ctggaccctg 240
 ttgtttatta ctttgcgtcc cggaattcc agctgcgcct gcgggaatat ttgggctgcc 300
 gccgggtgcc cagagacacc ctggacacgc gccgcgagag cctcttctcc gccaggacca 360
 cgtccgtgcg ctccgaggcc ggtgcgcacc ctgaagggat ggaggagacc accaggcccg 420
 gcctccagag gcaggagagt gtgttctgag tcccgggggc gcagc 465

<210> 50
 <211> 160
 <212> PRT
 <213> H.Sapiens

<400> 50

Leu Phe Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu Glu Ala His
 1 5 10 15

Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala Val Val Leu
 20 25 30

Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val Leu Leu Ala
 35 40 45

His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr His Val Tyr
 50 55 60

Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu Asp Pro Phe
 65 70 75 80

Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu Arg Glu Tyr
 85 90 95

Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr Arg Arg Glu

100

105

110

Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu Ala Gly Ala
 115 120 125

His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu Gln Arg Gln
 130 135 140

Glu Ser Val Phe Val Pro Gly Ala Gln Ala Ala Pro Pro Gly Leu Arg
 145 150 155 160

<210> 51
 <211> 603
 <212> DNA
 <213> H.Sapiens

<400> 51
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 ccggaaccca cagggcccccg tgggccatga gaggctcctg gacttgaacc tcaggacact 180
 cccactctgg ctgccggcag ggatggaagc tggatgagca ggcaggagct ggcagtgggg 240
 gtggagagcc ataggctatt ggggtggaca ggcttgggtg cctcatggga gctcccatg 300
 ggagctgtgg ccccttgggg cctcttattt ctcacccag gctttcccg gagaggttca 360
 agtcagaaga tgccccaaag atccacgtgg ccctgggtgg cagcctgttc ctctgaatc 420
 tggccttctt ggtcaatgtg gggagtggct caaaggggtc tgatgctgcc tgctgggccc 480
 ggggggctgt cttccactac ttctgctct gtgccttcac ctggatgggc cttgaagcct 540
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 agc 603

<210> 52
 <211> 198
 <212> PRT
 <213> H.Sapiens

<400> 52

Glu Thr Tyr Ser Ala Leu Tyr Pro Thr Phe Asn Ser Leu Cys Tyr Ser
 1 5 10 15

Pro Ala Ser Phe Ser Gly Leu Ile Phe Pro Ile Ile Leu Pro His Ile
 20 25 30

Asp Gln Gly Met Arg Leu Ala Gly Ser Gly Thr His Arg Ala Pro Trp
 35 40 45

Ala Met Arg Gly Ser Trp Thr Thr Ser Gly His Ser His Ser Gly Cys
 50 55 60

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Arg Gln Gly Trp Lys Leu Asp Glu Gln Ala Gly Ala Gly Ser Gly Gly
65 70 75 80

Gly Glu Pro Ala Ile Gly Val Asp Arg Leu Gly Cys Leu Met Gly Ala
85 90 95

Pro His Gly Ser Cys Gly Pro Leu Gly Pro Leu Ile Ser His Pro Arg
100 105 110

Leu Ser Arg Glu Arg Phe Lys Ser Glu Asp Ala Pro Lys Ile His Val
115 120 125

Ala Leu Gly Gly Ser Leu Phe Leu Leu Asn Leu Ala Phe Leu Val Asn
130 135 140

Val Gly Ser Gly Ser Lys Gly Ser Asp Ala Ala Cys Trp Ala Arg Gly
145 150 155 160

Ala Val Phe His Tyr Phe Leu Leu Cys Ala Phe Thr Trp Met Gly Leu
165 170 175

Glu Ala Phe His Leu Tyr Leu Leu Ala Val Arg Val Phe Asn Thr Tyr
180 185 190

Phe Gly His Tyr Phe Leu
195

<210> 53
<211> 335
<212> DNA
<213> H.Sapiens

<400> 53
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caaacacagc cagcacagcc ccaaagccaa acactatgta cagaatcacc cgggatcccg 120
gcgagaaggg gattttcaca caggacccat tcacgttcgc gtagcacagc tgcacagcca 180
ccagcaggga tgaattgctg ctcataacgc tggatatttac atatggagaa attttgcct 240
tggtgattat cacaaaaaat acaggattgt tcttgatttt cattgctcct gcggaaaaaa 300
acacatattc accaggatgc cagaggaaat gatca 335

<210> 54
<211> 111
<212> PRT
<213> H.Sapiens

<400> 54

Asp His Phe Leu Trp His Pro Gly Glu Tyr Val Phe Phe Ser Ala Gly
1 5 10 15

Ala Met Lys Ile Arg Asn Asn Pro Val Phe Phe Val Ile Ile Asn Lys
20 25 30

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Asp Lys Ile Ser Pro Tyr Val Asn Thr Ser Val Met Ser Ser Asn Ser
35 40 45

Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala Asn Val Asn Gly Ser
50 55 60

Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile
65 70 75 80

Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe Gly Asn Leu Leu Val
85 90 95

Met Ile Ser Ile Leu His Phe Lys Gln Leu His Ser Pro Thr Asn
100 105 110

<210> 55

<211> 586

<212> DNA

<213> H.Sapiens

<400> 55

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tatcctgaac ttcgtctatc caactgctta tatatgttca gaaaacaaat tcatggttgc 180
tgaactgttc tttaaaacct gaccagttac aataactttt attgctttcc taaaccatgg 240
gtaaaaataaa gcataaatca aaggattcat ggctgagtta taataagcac accaacagca 300
tcataaatac aggcaggggt tataaagccc ataaaggcat caattaatga atcaatgcta 360
tatggtaacc atgaaatcat aaatgctacc actgtgaccc ccagggtttt agctgctttt 420
ctctctctcc tggccactct ggctttgtaa ctctctgagg atgattctgt cttgctacca 480
gtattttcta tctttttcgc ctgtcgtcta gccacaagaa atatgttacc atacagaatt 540
atcataataa aggtaggtat aaagaaggat agaaaatctg tcaaca 586

<210> 56

<211> 190

<212> PRT

<213> H.Sapiens

<400> 56

Leu Thr Asp Phe Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile
1 5 10 15

Leu Tyr Gly Asn Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile
20 25 30

Glu Asn Thr Gly Ser Lys Thr Glu Ser Ser Ser Glu Ser Tyr Lys Ala
35 40 45

Arg Val Ala Arg Arg Glu Arg Lys Ala Ala Lys Thr Leu Gly Val Thr

50

55

60

Val Val Ala Phe Met Ile Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu
65 70 75 80

Ile Asp Ala Phe Met Gly Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile
85 90 95

Cys Cys Trp Cys Ala Tyr Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr
100 105 110

Ala Leu Phe Tyr Pro Trp Phe Arg Lys Ala Ile Lys Val Ile Val Thr
115 120 125

Gly Gln Val Leu Lys Asn Ser Ser Ala Thr Met Asn Leu Phe Ser Glu
130 135 140

His Ile Ala Val Gly Thr Lys Phe Arg Ile Pro Leu Lys Leu Pro Ser
145 150 155 160

Glu Met Ser Phe Lys Ser Ser Lys Thr Met Asn Glu Gln Ile Asn Cys
165 170 175

Ser Ser Asn Lys Gln Ile Asn Val Phe Gln Ser Cys Asp Val
180 185 190

<210> 57

<211> 976

<212> DNA

<213> H.Sapiens

<400> 57

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tggtaggaaa cgggtttgtg ctctggctcc tgggcttccg catgcgcagg aacgccttct 120
ctgtctacgt cctcagcctg gccggggccg acttctctct cctctgcttc cagattataa 180
attgcctggt gtacctcagt aacttcttct gttccatctc catcaatttc cctagcttct 240
tcaccactgt gatgacctgt gcctaccttg caggcctgag catgctgagc accgtcagca 300
ccgagcgtg cctgtccgtc ctgtggccca tctggtatcg ctgccgccgc ccagacacc 360
tgtcagcggg cgtgtgtgtc ctgctctggg cctgtccct actgctgagc atcttggaag 420
ggaagtctg tggcttctta tttagtgatg gtgactctgg ttggtgtcag acatttgatt 480
tcatcactgc agcgtggctg atttttttat tcatggttct ctgtgggtcc agtctggccc 540
tgctggtcag gatcctctgt ggctccaggg gtctgccact gaccaggctg tacctgacca 600
tctgctcac agtgctggtg tccctctctc gccgcctgcc ctttggcatt cagtggttcc 660
taatattatg gatctggaag gattctgatg tcttattttg tcatattcat ccagtttcag 720
ttgtcctgtc atctcttaac agcagtgcc accccatcat ttacttcttc gtgggctctt 780
ttaggaagca gtggcggstg cagcacccga tcctcaagct ggctctccag agggctctgc 840

aggacattgc tgaggtggat cacagtgaag gatgcttccg tcagggcacg cggagattca 900
 aagaagcatt ctggtgtagg gatggacccc tctacttcca tcatatatat gtggctttga 960
 gaggcaactt tgcccc 976

<210> 58
 <211> 324
 <212> PRT
 <213> H.Sapiens
 <220>
 <221> UNSURE
 <222> (266)..(266)
 <223> Xaa is Unknown

<400> 58

Cys	Gly	Lys	Glu	Thr	Leu	Ile	Pro	Val	Phe	Leu	Ile	Leu	Phe	Ile	Ala	1	5	10	15
Leu	Val	Gly	Leu	Val	Gly	Asn	Gly	Phe	Val	Leu	Trp	Leu	Leu	Gly	Phe	20	25	30	
Arg	Met	Arg	Arg	Asn	Ala	Phe	Ser	Val	Tyr	Val	Leu	Ser	Leu	Ala	Gly	35	40	45	
Ala	Asp	Phe	Leu	Phe	Leu	Cys	Phe	Gln	Ile	Ile	Asn	Cys	Leu	Val	Tyr	50	55	60	
Leu	Ser	Asn	Phe	Phe	Cys	Ser	Ile	Ser	Ile	Asn	Phe	Pro	Ser	Phe	Phe	65	70	75	80
Thr	Thr	Val	Met	Thr	Cys	Ala	Tyr	Leu	Ala	Gly	Leu	Ser	Met	Leu	Ser	85	90	95	
Thr	Val	Ser	Thr	Glu	Arg	Cys	Leu	Ser	Val	Leu	Trp	Pro	Ile	Trp	Tyr	100	105	110	
Arg	Cys	Arg	Arg	Pro	Arg	His	Leu	Ser	Ala	Val	Val	Cys	Val	Leu	Leu	115	120	125	
Trp	Ala	Leu	Ser	Leu	Leu	Leu	Ser	Ile	Leu	Glu	Gly	Lys	Phe	Cys	Gly	130	135	140	
Phe	Leu	Phe	Ser	Asp	Gly	Asp	Ser	Gly	Trp	Cys	Gln	Thr	Phe	Asp	Phe	145	150	155	160
Ile	Thr	Ala	Ala	Trp	Leu	Ile	Phe	Leu	Phe	Met	Val	Leu	Cys	Gly	Ser	165	170	175	
Ser	Leu	Ala	Leu	Leu	Val	Arg	Ile	Leu	Cys	Gly	Ser	Arg	Gly	Leu	Pro	180	185	190	
Leu	Thr	Arg	Leu	Tyr	Leu	Thr	Ile	Leu	Leu	Thr	Val	Leu	Val	Ser	Leu	195	200	205	

Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Phe Leu Ile Leu Trp Ile
 210 215 220

Trp Lys Asp Ser Asp Val Leu Phe Cys His Ile His Pro Val Ser Val
 225 230 235 240

Val Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe
 245 250 255

Val Gly Ser Phe Arg Lys Gln Trp Arg Xaa Gln His Pro Ile Leu Lys
 260 265 270

Leu Ala Leu Gln Arg Ala Leu Gln Asp Ile Ala Glu Val Asp His Ser
 275 280 285

Glu Gly Cys Phe Arg Gln Gly Thr Arg Arg Phe Lys Glu Ala Phe Trp
 290 295 300

Cys Arg Asp Gly Pro Leu Tyr Phe His His Ile Tyr Val Ala Leu Arg
 305 310 315 320

Gly Asn Phe Ala

<210> 59
 <211> 578
 <212> DNA
 <213> H.Sapiens

<400> 59
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 gtaacagggt accaaagggtg ttcagagcag cataatgggtc tagaaacgat gtaagcttca 120
 tggatctgat tctcaatgga acaactgatt gaaagcaggc tgagattcga tcttgaatga 180
 ccctcaagat atggaagggt aaaaaacata cgtaaaatgc aaggagtagc agaattggtta 240
 gccttcgtgc tttctgctta aggcagctgt cagtttgcag tccatgggtc aaagtgtgga 300
 taatcgtggt atagcaaagt gtcactatca ccaaggggag gcagaaagta cttgcagtca 360
 aaatcagggt gtaccactta atagtattga gttcatccga actggtgagg tcgagacagg 420
 ctgatctggt ggtcctgttg gttgatgtga tcaagaaggc catcggaatg acagctacca 480
 gtgaaatgat ccacaccaca gcacaggcta caactgcaca tcgagttttg tgaatggaaa 540
 agcagctcat tgggtgaatg atcacacagt agcgggaag 578

<210> 60
 <211> 192
 <212> PRT
 <213> H.Sapiens

<400> 60

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Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile His
 1 5 10 15
 Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile Ser
 20 25 30
 Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn Arg
 35 40 45
 Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu Asn
 50 55 60
 Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys Leu
 65 70 75 80
 Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr Leu
 85 90 95
 Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg Arg
 100 105 110
 Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro Phe
 115 120 125
 His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln Ser
 130 135 140
 Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu Asp
 145 150 155 160
 His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
 165 170 175
 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
 180 185 190

<210> 61
 <211> 872
 <212> DNA
 <213> H.Sapiens

<400> 61
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 atctgtttct catggtctcc tgtctgtctc tctctctctc cctctttct ctctcctgc 120
 tctttctcat cccctccatt tctgtgtcaa tctcaatcca tttatatcgg tggccacttt 180
 tctatctctt tgttctatct ctctctctct ctctttccca ctttgtctct gcacgcctgt 240
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 tctctgtctc tctgtgtctg tgtctcccc gctattccc atttgaggt gcaatgtagc 360
 aggacaactc atggagcccc cccgggcccc tcgagtaccg gactggctga ccccctaggg 420
 ttggcagtag cccctgaccc tcagtatggc caacactacc ggagagcctg aggaggtgag 480
 cggcgctctg tccccaccgt ccgcatcagc ttatgtgaag ctggtactgc tgggactgat 540

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tatgtgcgtg agcctggcgg gtaacgccat cttgtccctg ctggtgctca aggagcgggc 600
cctgcacaag gctccttact acttctctgct ggacctgtgc ctggccgatg gcatacgctc 660
tgccgtctgc ttcccctttg tgctggcttc tgtgcgccac ggctcttcat ggaccttcag 720
tgcaactcagc tgcaagattg tggcctttat ggccgtgctc ttttgcttcc atgcggcctt 780
catgctgttc tgcacacagc tcacccgcta catggccatc gccaccacc gcttctacgc 840
caagcgcgtg acactctgga catgcgcggc tg 872

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<210> 62
 <211> 143
 <212> PRT
 <213> H.Sapiens

<400> 62

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Met Ala Asn Thr Thr Gly Glu Pro Glu Glu Val Ser Gly Ala Leu Ser
1          5          10          15
Pro Pro Ser Ala Ser Ala Tyr Val Lys Leu Val Leu Leu Gly Leu Ile
          20          25          30
Met Cys Val Ser Leu Ala Gly Asn Ala Ile Leu Ser Leu Leu Val Leu
          35          40          45
Lys Glu Arg Ala Leu His Lys Ala Pro Tyr Tyr Phe Leu Leu Asp Leu
          50          55          60
Cys Leu Ala Asp Gly Ile Arg Ser Ala Val Cys Phe Pro Phe Val Leu
          65          70          75          80
Ala Ser Val Arg His Gly Ser Ser Trp Thr Phe Ser Ala Leu Ser Cys
          85          90          95
Lys Ile Val Ala Phe Met Ala Val Leu Phe Cys Phe His Ala Ala Phe
          100          105          110
Met Leu Phe Cys Ile Ser Val Thr Arg Tyr Met Ala Ile Ala His His
          115          120          125
Arg Phe Tyr Ala Lys Arg Met Thr Leu Trp Thr Cys Ala Ala Glu
          130          135          140

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<210> 63
 <211> 962
 <212> DNA
 <213> H.Sapiens

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<400> 63
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tgatttactc ttttattttt cctcctaggt ttctgggata agtatgtgca aataaaaaat 180

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aaacatgaga aggaactgta acctgattat ggatttggga aaaagataaa tcaacacaca      240
aagggaagaa taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat      300
taatatttcc tgtgtgaaaa acaactggtc aaatgatgtc cgtgcttccc tgtacagttt      360
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acacttcaaaa caacttcata ccccaacaaa ttggctcatt cattccatgg ccactgtgga      480
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ctccattttc catttgcctt tcatctccat tgaccgctac tatgctgtgt gtgatccact      660
gagatataaa gccaagatga atatcttggt tatttgtgtg atgatcttca ttagttggag      720
tgtccctgct gtttttgcac ttggaatgat ctttctggag ctaaaacttca aaggcgctga      780
agagatatat taaaaacatg ttcactgcag aggaggttgc tctgtcttct ttagcaaaat      840
atctggggta ctgaccttta tgacttcttt ttatatacct ggatctatta tgttatgtgt      900
ctattacaga atatatctta tcgctaaaga acaggcaaga ttaattagtg atgccaatca      960
ga

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<210> 64
<211> 238
<212> PRT
<213> H.Sapiens

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<400> 64

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Arg Glu Lys Thr Asp Gln Pro Ser Gly Met Met Pro Phe Cys His Asn
1          5          10          15
Ile Ile Asn Ile Ser Cys Val Lys Asn Asn Trp Ser Asn Asp Val Arg
20          25          30
Ala Ser Leu Tyr Ser Leu Met Val Leu Ile Ile Leu Thr Thr Leu Val
35          40          45
Gly Asn Leu Ile Val Ile Val Ser Ile Ser His Phe Lys Gln Leu His
50          55          60
Thr Pro Thr Asn Trp Leu Ile His Ser Met Ala Thr Val Asp Phe Leu
65          70          75          80
Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val Arg Ser Ala Glu His
85          90          95
Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile His Thr Ser Thr Asp
100         105         110
Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu Ser Phe Ile Ser Ile

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115

120

125

Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg Tyr Lys Ala Lys Met
 130 135 140

Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile Ser Trp Ser Val Pro
 145 150 155 160

Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu Leu Asn Phe Lys Gly
 165 170 175

Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys Arg Gly Gly Cys Ser
 180 185 190

Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr Phe Met Thr Ser Phe
 195 200 205

Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr Tyr Arg Ile Tyr Leu
 210 215 220

Ile Ala Lys Glu Gln Ala Arg Leu Ile Ser Asp Ala Asn Gln
 225 230 235

<210> 65
 <211> 1018
 <212> DNA
 <213> H.Sapiens

<400> 65
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 aagaaccaat gtcttgctca gatagaagca agatactcag acttagtttc tctgtagctc 120
 ctgcttttta ttattcctgg ttggattgca ccactactca gtttctatgt tataatactg 180
 attataaaac atgggagggg aataactttg tattggtttt tatggataat ttattatgtg 240
 tcctagactc tggccttgctc aaaagaagga cgtaagaagg cacgatgtat tatacttggg 300
 aatgatagaa gagactgacc tggatatttc acccggaaga gggaaaggat tttaactaca 360
 aatacaggaa tccagcagat ggcacagag aacactataa aaaagaaacg atttgcaaca 420
 gccacctctc ttccaaaaca attccttact tctgtggtct gcaaggcggg tttttgaatg 480
 gaacagaaca tagtaataata ggaaaacaca atgatgagaa aagccagcaa gttcacacct 540
 gttggggaaa agcacacttt taacatctca ggcgtaaaag tcaacagtaa aattactgtg 600
 gtacagggtg agtatccctt acccaaaatg tttgaaacca gaaatgtttt ggatttcgga 660
 tttcggaata ttacacatt cataatgata tatcttgga atggttccca agtctaaaca 720
 caaaatttat ttatgtttca tatacacctt atacacatag tctgaaagta attttgtaca 780
 atattttaaa taattttggg catgaaacaa agtttgcata cattgaacca tcagacagca 840
 aaagcttcag gtgtggaatt ttccacttgt ggcacatgt tgatgctcaa aaagttccat 900

atttttagagc atttcaaatt ttggattttc aaattacaaa tgcttaacct gtacttagat 960
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<210> 66
 <211> 327
 <212> PRT
 <213> H.Sapiens

<400> 66

Tyr Ile Lys Glu Cys Phe Leu Lys Val Pro Val Glu Glu Ala Leu Tyr
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 Leu Thr Ser Lys Tyr Arg Leu Ser Ile Cys Asn Leu Lys Ile Gln Asn
 20 25 30
 Leu Lys Cys Ser Lys Ile Trp Asn Phe Leu Ser Ile Asn Met Met Pro
 35 40 45
 Gln Val Glu Asn Ser Thr Pro Glu Ala Phe Ala Val Trp Phe Asn Val
 50 55 60
 Cys Lys Leu Cys Phe Met Pro Lys Ile Ile Asn Ile Val Gln Asn Tyr
 65 70 75 80
 Phe Gln Thr Met Cys Ile Arg Cys Ile Asn Ile Asn Lys Phe Cys Val
 85 90 95
 Thr Trp Glu Pro Phe Pro Arg Tyr Ile Ile Met Asn Val Ile Phe Arg
 100 105 110
 Asn Pro Lys Ser Lys Thr Phe Leu Val Ser Asn Ile Leu Gly Lys Gly
 115 120 125
 Tyr Ser Thr Cys Thr Thr Val Ile Leu Leu Leu Thr Phe Thr Pro Glu
 130 135 140
 Met Leu Lys Val Cys Phe Ser Pro Thr Gly Val Asn Leu Leu Ala Phe
 145 150 155 160
 Leu Ile Ile Val Phe Ser Tyr Ile Thr Met Phe Cys Ser Ile Gln Lys
 165 170 175
 Thr Ala Leu Gln Thr Thr Glu Val Arg Asn Cys Phe Gly Arg Glu Val
 180 185 190
 Ala Val Ala Asn Arg Phe Phe Phe Ile Val Phe Ser Asp Ala Ile Cys
 195 200 205
 Trp Ile Pro Val Phe Val Val Lys Ile Leu Ser Leu Phe Arg Val Glu
 210 215 220
 Ile Pro Gly Gln Ser Leu Leu Ser Phe Pro Ser Ile Ile His Arg Ala
 225 230 235 240
 Phe Leu Arg Pro Ser Phe Asp Lys Ala Arg Val Asp Thr Ile Ile His
 245 250 255

Lys Asn Gln Tyr Lys Val Ile Ser Leu Pro Cys Phe Ile Ile Ser Ile
 260 265 270

Ile Lys Lys Leu Ser Ser Gly Ala Ile Gln Pro Gly Ile Ile Lys Ser
 275 280 285

Arg Ser Tyr Arg Glu Thr Lys Ser Glu Tyr Leu Ala Ser Ile Ala Arg
 290 295 300

His Trp Phe Phe Thr Arg Ser Met His Lys Thr Ile Lys Ile Tyr Met
 305 310 315 320

Pro Arg Phe His Pro Gly Leu
 325

<210> 67

<211> 1251

<212> DNA

<213> H.Sapiens

<400> 67

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gagccgatgg cagaggccca gtcacagatg gatcctgtgg cccagcctca ggtgaacccc	1080
aactccagc cacgatcgga tcccacagct cagccacagc tgaaccctac ggcccagcca	1140

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<210> 68
 <211> 417
 <212> PRT
 <213> H.Sapiens
 <400> 68

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 Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp Thr Val
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 Phe Leu Val Ala Leu Leu Leu Leu Gly Leu Pro Ala Asn Gly Leu Met
 35 40 45
 Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr Arg Leu
 50 55 60
 Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe Leu Ala
 65 70 75 80
 Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His Trp Pro
 85 90 95
 Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly Val Ser
 100 105 110
 Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp Arg Cys
 115 120 125
 Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro Val Arg
 130 135 140
 Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr Leu Phe
 145 150 155 160
 Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp Tyr Asp
 165 170 175
 Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser Leu Arg
 180 185 190
 Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu Leu Val
 195 200 205
 Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg Thr Cys His Arg Gln
 210 215 220
 Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg Thr Ile
 225 230 235 240
 Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala Gln Leu

245

250

255

Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu Leu Trp
 260 265 270

Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser Cys Leu
 275 280 285

Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr Leu Leu
 290 295 300

Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu Arg Pro
 305 310 315 320

Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser Glu Gly
 325 330 335

Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met Asp Pro
 340 345 350

Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser Asp Pro
 355 360 365

Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser Asp Pro
 370 375 380

Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser Asp Ser
 385 390 395 400

Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln Thr Pro Ala Pro Ala
 405 410 415

Ala

<210> 69
 <211> 659
 <212> DNA
 <213> H.Sapiens

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 catctagtac cgctgccacc accccacaca cctgtcagca gtcgtgtgtc ctgctctggg 120
 ccctgtccct gctgcagagc atcctggaat ggatgttctg tggcttcctg tctagtgggtg 180
 ctgattctgt ttggtgtgaa acatcagatt tcatcacagt cacatggctg atttttttat 240
 gtgtggttct ctgcgggtcc agcccggttc tgctggtcag gatcctttgt ggatcccgga 300
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 gtgacctgcc ctttggcatt cagtgattcc tatttttctg gatccacgtg gatttgtcac 420
 gttcgtctag tttccatttt cctgtccact cttaacagca gtgccaaccc cattattttac 480
 ttcttcatgg gctcctttag gcagcttcaa aacaggaaga ctctctagct gggtctccag 540

aggggctctgc aggacacgcc tgagggtggaa gaaggcagat ggcggctttc tgaggaaacc 600
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<210> 70
 <211> 213
 <212> PRT
 <213> H.Sapiens

<400> 70

Tyr Arg Pro Glu His Ala Gly Leu His Gln His Gln Ala Leu Pro Val
 1 5 10 15
 His Pro Val Ala His Leu Val Pro Leu Pro Pro Pro His Thr Pro Val
 20 25 30
 Ser Ser Arg Val Ser Cys Ser Gly Pro Cys Pro Cys Cys Arg Ala Ser
 35 40 45
 Trp Asn Gly Cys Ser Val Ala Ser Cys Leu Val Val Leu Ile Leu Phe
 50 55 60
 Gly Val Lys His Gln Ile Ser Ser Gln Ser His Gly Phe Phe Tyr Val
 65 70 75 80
 Trp Phe Ser Ala Gly Pro Ala Arg Phe Cys Trp Ser Gly Ser Phe Val
 85 90 95
 Asp Pro Gly Arg Cys Pro Pro Gly Cys Thr Pro Ser Cys Ser Glu Cys
 100 105 110
 Trp Ser Ser Ser Ser Val Thr Cys Pro Leu Ala Phe Ser Asp Ser Tyr
 115 120 125
 Phe Ser Gly Ser Thr Trp Ile Cys His Val Arg Leu Val Ser Ile Phe
 130 135 140
 Leu Ser Thr Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met
 145 150 155 160
 Gly Ser Phe Arg Gln Leu Gln Asn Arg Lys Thr Leu Leu Val Leu Gln
 165 170 175
 Arg Ala Leu Gln Asp Thr Pro Glu Val Glu Glu Gly Arg Trp Arg Leu
 180 185 190
 Ser Glu Glu Thr Leu Glu Leu Ser Ser Arg Leu Gly Pro Gly Arg Ala
 195 200 205
 Ser Ala Leu Ser Val
 210

<210> 71
 <211> 559
 <212> DNA
 <213> H.Sapiens

<400> 71
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 cccacacatg gtgcaacaca gcagagccag cagcaccgct gccaccagcc acagcgtccg 180
 gcacaagtgg cggctgggct ccccgaagaa ctgggtgcag gcgccgctga gcagcaggtg 240
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 gaagcccggg aagtccagcc ggccttgca caagtcgggg acgatggcca ccatgtggca 480
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 gtagacattg gagctgagc 559

<210> 72
 <211> 211
 <212> PRT
 <213> H.Sapiens

<400> 72
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 Val Ala Cys Ala Asp Leu Ile Phe Leu Gly Cys His Met Val Ala Ile
 20 25 30
 Val Pro Asp Leu Leu Gln Gly Arg Leu Asp Phe Pro Gly Phe Val Gln
 35 40 45
 Thr Ser Leu Ala Thr Leu Arg Phe Phe Cys Tyr Ile Val Gly Leu Ser
 50 55 60
 Leu Leu Ala Ala Val Ser Val Glu Gln Cys Leu Ala Ala Leu Phe Pro
 65 70 75 80
 Ala Trp Tyr Ser Cys Arg Arg Pro Arg His Leu Thr Thr Cys Val Cys
 85 90 95
 Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Thr Thr Cys Val
 100 105 110
 Cys Ala Leu Thr Trp Ala Leu Cys Leu Leu Leu His Leu Leu Leu Ser
 115 120 125
 Gly Ala Cys Thr Leu Leu Leu Ser Gly Ala Cys Thr Gln Phe Phe Gly
 130 135 140
 Glu Pro Ser Arg His Leu Cys Arg Thr Leu Trp Leu Val Ala Ala Val
 145 150 155 160

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Leu Leu Ala Leu Leu Cys Cys Thr Met Cys Gly Ala Ser Leu Met Leu
 165 170 175

Leu Leu Arg Val Glu Arg Gly Pro Gln Arg Pro Pro Pro Arg Gly Phe
 180 185 190

Pro Gly Leu Ile Leu Leu Thr Val Leu Leu Phe Ser Ser Ala Ala Cys
 195 200 205

Leu Arg His
 210

<210> 73
 <211> 1008
 <212> DNA
 <213> H.Sapiens

<400> 73
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 actaacacac tagtggctgt ggctgtgctg ctgttgatcc acaagaatga tgggtgtcagt 120
 ctctgcttca ccttgaatct ggctgtggct gacaccttga ttggtgtggc catctctggc 180
 ctactcacag accagctctc cagcccttct cggcccacac agaagaccct gtgcagcctg 240
 cggatggcat ttgtcacttc ctccgcagct gcctctgtcc tcacgggtcat gctgatcacc 300
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 tttcaccctc acttcgtgct gacctctcc tgcgttggct tcttcccagc catgctcctc 540
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 aagatggaac atgcaggagc catggctgga ggttatcgat cccacaggac tcccagcgac 660
 ttcaaagctc tccgtactgt gtctgttctc attgggagct ttgctctatc ctggaccccc 720
 ttccttatca ctggcattgt gcagggtggc tgccaggagt gtcacctcta cctagtgtgtg 780
 gaacggtacc tgtggctgct cggcgtgggc aactccctgc tcaaccact catctatgcc 840
 tattggcaga aggaggtgcg actgcagctc taccacatgg ccctaggagt gaagaagggtg 900
 ctcacctcat tctcctctt tctctcgcc aggaattgtg gccagagag gccagggaa 960
 agttcctgtc acatcgtcac tatctccagc tcagagtttg atggctaa 1008

<210> 74
 <211> 335
 <212> PRT
 <213> H.Sapiens

<400> 74

Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala Ser
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 Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu Leu
 20 25 30
 Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu Ala
 35 40 45
 Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr Asp
 50 55 60
 Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser Leu
 65 70 75 80
 Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr Val
 85 90 95
 Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe Arg
 100 105 110
 Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala Gly
 115 120 125
 Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile Pro
 130 135 140
 Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala Val
 145 150 155 160
 Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe Pro
 165 170 175
 Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile Ala
 180 185 190
 Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala Met
 195 200 205
 Ala Gly Gly Tyr Arg Ser Pro Arg Thr Pro Ser Asp Phe Lys Ala Leu
 210 215 220
 Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala Leu Ser Trp Thr Pro
 225 230 235 240
 Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys Gln Glu Cys His Leu
 245 250 255
 Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu Gly Val Gly Asn Ser
 260 265 270
 Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln Lys Glu Val Arg Leu
 275 280 285
 Gln Leu Tyr His Met Ala Leu Gly Val Lys Lys Val Leu Thr Ser Phe
 290 295 300
 Leu Leu Phe Leu Ser Ala Arg Asn Cys Gly Pro Glu Arg Pro Arg Glu

305

310

315

320

Ser Ser Cys His Ile Val Thr Ile Ser Ser Ser Glu Phe Asp Gly
 325 330 335

<210> 75
 <211> 2137
 <212> DNA
 <213> H.Sapiens

<400> 75
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 aagcgttgca tctgtttacc tggagaccct ctgagctctc acctgtact tctgccgtg 180
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 tgtactcgtt ggtggcggcg gtcagcatcc cgggcaacct cttctctctg tgggtgctgt 360
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<210> 76
<211> 359
<212> PRT
<213> H.Sapiens

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<400> 76

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Leu Arg Asn Pro Ala Ile Ala Val Ala Leu Pro Val Val Tyr Ser Leu
          20          25          30
Val Ala Ala Val Ser Ile Pro Gly Asn Leu Phe Ser Leu Trp Val Leu
          35          40          45
Cys Arg Arg Met Gly Pro Arg Ser Pro Ser Val Ile Phe Met Ile Asn
          50          55          60
Leu Ser Val Thr Asp Leu Met Leu Ala Ser Val Leu Pro Phe Gln Ile
          65          70          75          80
Tyr Tyr His Cys Asn Arg His His Trp Val Phe Gly Val Leu Leu Cys
          85          90          95
Asn Val Val Thr Val Ala Phe Tyr Ala Asn Met Tyr Ser Ser Ile Leu
          100          105          110
Thr Met Thr Cys Ile Ser Val Glu Arg Phe Leu Gly Val Leu Tyr Pro
          115          120          125
Leu Ser Ser Lys Arg Trp Arg Arg Arg Arg Tyr Ala Val Ala Ala Cys
          130          135          140

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Ala Gly Thr Trp Leu Leu Leu Leu Thr Ala Leu Ser Pro Leu Ala Arg
 145 150 155 160

Thr Asp Leu Thr Tyr Pro Val His Ala Leu Gly Ile Ile Thr Cys Phe
 165 170 175

Asp Val Leu Lys Trp Thr Met Leu Pro Ser Val Ala Met Trp Ala Val
 180 185 190

Phe Leu Phe Thr Ile Phe Ile Leu Leu Phe Leu Ile Pro Phe Val Ile
 195 200 205

Thr Val Ala Cys Tyr Thr Ala Thr Ile Leu Lys Leu Leu Arg Thr Glu
 210 215 220

Glu Ala His Gly Arg Glu Gln Arg Arg Arg Ala Val Gly Leu Ala Ala
 225 230 235 240

Val Val Leu Leu Ala Phe Val Thr Cys Phe Ala Pro Asn Asn Phe Val
 245 250 255

Leu Leu Ala His Ile Val Ser Arg Leu Phe Tyr Gly Lys Ser Tyr Tyr
 260 265 270

His Val Tyr Lys Leu Thr Leu Cys Leu Ser Cys Leu Asn Asn Cys Leu
 275 280 285

Asp Pro Phe Val Tyr Tyr Phe Ala Ser Arg Glu Phe Gln Leu Arg Leu
 290 295 300

Arg Glu Tyr Leu Gly Cys Arg Arg Val Pro Arg Asp Thr Leu Asp Thr
 305 310 315 320

Arg Arg Glu Ser Leu Phe Ser Ala Arg Thr Thr Ser Val Arg Ser Glu
 325 330 335

Ala Gly Ala His Pro Glu Gly Met Glu Gly Ala Thr Arg Pro Gly Leu
 340 345 350

Gln Arg Gln Glu Ser Val Phe
 355

<210> 77
 <211> 1197
 <212> DNA
 <213> H.Sapiens

<400> 77
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 tcggatctgc tggcaggcgc cgcctacgcc gccaacatcc tactgtcggg gccgctcacg 300
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 ttctgtggga tcttgccgc tatctgtgca ctctacgcgc gcctctactg ccaggtaagg 660
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 agcggctcgg agcgtctatc gcccagcgcg gacgggctgg acaccagcgg ctccacaggc 1140
 agccccggtg caccacagc cgcccggact ctggtatcag aaccggctgc agactga 1197

<210> 78
 <211> 398
 <212> PRT
 <213> H.Sapiens

<400> 78

Met Glu Ser Gly Leu Leu Arg Pro Ala Pro Val Ser Glu Val Ile Val
 1 5 10 15
 Leu His Tyr Asn Tyr, Thr Gly Lys Leu Arg Gly Ala Arg Tyr Gln Pro
 20 25 30
 Gly Ala Gly Leu Arg Ala Asp Ala Val Val Cys Leu Ala Val Cys Ala
 35 40 45
 Phe Ile Val Leu Glu Asn Leu Ala Val Leu Leu Val Leu Gly Arg His
 50 55 60
 Pro Arg Phe His Ala Pro Met Phe Leu Leu Leu Gly Ser Leu Thr Leu
 65 70 75 80
 Ser Asp Leu Leu Ala Gly Ala Ala Tyr Ala Ala Asn Ile Leu Leu Ser
 85 90 95
 Gly Pro Leu Thr Leu Lys Leu Ser Pro Ala Leu Trp Phe Ala Arg Glu
 100 105 110
 Gly Gly Val Phe Val Ala Leu Thr Ala Ser Val Leu Ser Leu Leu Ala

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115

120

125

Ile Ala Leu Glu Arg Ser Leu Thr Met Ala Arg Arg Gly Pro Ala Pro
 130 135 140
 Val Ser Ser Arg Gly Arg Thr Leu Ala Met Ala Ala Ala Ala Trp Gly
 145 150 155 160
 Val Ser Leu Leu Leu Gly Leu Leu Pro Ala Leu Gly Trp Asn Cys Leu
 165 170 175
 Gly Arg Leu Asp Ala Cys Ser Thr Val Leu Pro Leu Tyr Ala Lys Ala
 180 185 190
 Tyr Val Leu Phe Cys Val Leu Ala Phe Val Gly Ile Leu Ala Ala Ile
 195 200 205
 Cys Ala Leu Tyr Ala Arg Ile Tyr Cys Gln Val Arg Ala Asn Ala Arg
 210 215 220
 Arg Leu Pro Ala Arg Pro Gly Thr Ala Gly Thr Thr Ser Thr Arg Ala
 225 230 235 240
 Arg Arg Lys Pro Arg Ser Leu Ala Leu Leu Arg Thr Leu Ser Val Val
 245 250 255
 Leu Leu Ala Phe Val Ala Cys Trp Gly Pro Leu Phe Leu Leu Leu Leu
 260 265 270
 Leu Asp Val Ala Cys Pro Ala Arg Thr Cys Pro Val Leu Leu Gln Ala
 275 280 285
 Asp Pro Phe Leu Gly Leu Ala Met Ala Asn Ser Leu Leu Asn Pro Ile
 290 295 300
 Ile Tyr Thr Leu Thr Asn Arg Asp Leu Arg His Ala Leu Leu Arg Leu
 305 310 315 320
 Val Cys Cys Gly Arg His Ser Cys Gly Arg Asp Pro Ser Gly Ser Gln
 325 330 335
 Gln Ser Ala Ser Ala Ala Glu Ala Ser Gly Gly Leu Arg Arg Cys Leu
 340 345 350
 Pro Pro Gly Leu Asp Gly Ser Phe Ser Gly Ser Glu Arg Ser Ser Pro
 355 360 365
 Gln Arg Asp Gly Leu Asp Thr Ser Gly Ser Thr Gly Ser Pro Gly Ala
 370 375 380
 Pro Thr Ala Ala Arg Thr Leu Val Ser Glu Pro Ala Ala Asp
 385 390 395

<210> 79

<211> 1041

<212> DNA

<213> H.Sapiens

<400> 79

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tgcttcaca tgaagacctg gaagcccagc actgtttacc ttttcaattt ggccgtggct      180
gatttcctcc ttatgatctg cctgcctttt cggacagact attacctcag acgtagacac      240
tgggcttttg gggacattcc ctgccgagtg gggctcttca cgttggccat gaacagggcc      300
gggagcatcg tgttccttac ggtggtggtt gcggacaggt atttcaaagt ggtccacccc      360
caccacgcgg tgaacactat ctccaccggg gtggcggttg gcatcgtctg caccctgtgg      420
gccctgggtc tcttggaac agtgtatctt ttgctggaga accatctctg cgtgcaagag      480
acggccgtct cctgtgagag cttcatcatg gagtcggcca atggctggca tgacatcatg      540
ttccagctgg agttctttat gccctcggc atcatcttat tttgctcctt caagattggt      600
tggagcctga ggcggaggca gcagctggcc agacaggctc ggatgaagaa ggcgacccgg      660
ttcatcatgg tggtggaac tgtgttcac acatgctacc tgcccagcgt gtctgctaga      720
ctctatttcc tctggacggt gccctcgagt gcctgcgac cctctgtcca tggggccctg      780
cacataaccc tcagcttcac ctacatgaac agcatgctgg atcccctggt gtattatatt      840
tcaagcccct cctttcccaa attctacaac aagctcaaaa tctgcagtct gaaacccaag      900
cagccaggac actcaaaaac acaaaggccg gaagagatgc caatttcgaa cctcggtcgc      960
aggagtgc tcaagtgtggc aaatagtttc caaagccagt ctgatgggca atgggatccc     1020
cacattgttg agtggcactg a                                             1041

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<210> 80
<211> 346
<212> PRT
<213> H.Sapiens

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<400> 80

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Met Tyr Asn Gly Ser Cys Cys Arg Ile Glu Gly Asp Thr Ile Ser Gln
1          5          10          15
Val Met Pro Pro Leu Leu Ile Val Ala Phe Val Leu Gly Ala Leu Gly
          20          25          30
Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys
          35          40          45
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu
          50          55          60
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr Tyr Leu Arg Arg Arg His
65          70          75          80

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Trp Ala Phe Gly Asp Ile Pro Cys Arg Val Gly Leu Phe Thr Leu Ala
 85 90 95
 Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp
 100 105 110
 Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser
 115 120 125
 Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile
 130 135 140
 Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu
 145 150 155 160
 Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp
 165 170 175
 His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile
 180 185 190
 Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln
 195 200 205
 Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val
 210 215 220
 Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg
 225 230 235 240
 Leu Tyr Phe Leu Trp Thr Val Pro Ser Ser Ala Cys Asp Pro Ser Val
 245 250 255
 His Gly Ala Leu His Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met
 260 265 270
 Leu Asp Pro Leu Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Lys Phe
 275 280 285
 Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His
 290 295 300
 Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg
 305 310 315 320
 Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly
 325 330 335
 Gln Trp Asp Pro His Ile Val Glu Trp His
 340 345

<210> 81
 <211> 2525
 <212> DNA
 <213> H.Sapiens

<400> 81
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tggtgggtgt	catttccatt	cttttctctc	tggtgaaaat	gaacacccgg	tcagtgacca	180
ccatggcggg	cattaacttg	gtgggtggcc	acagcgtttt	tctgctgaca	gtgccatttc	240
gcttgaccta	cctcatcaag	aagacttgga	tgtttgggct	gcccttctgc	aaatttgtga	300
gtgccatgct	gcacatccac	atgtacctca	cgttcctatt	ctatgtgggtg	atcctgggtca	360
ccagatacct	catcttcttc	aagtgcaaag	acaaagtgga	attctacaga	aaactgcatg	420
ctgtggctgc	cagtgcctgg	atgtggacgc	tggtgattgt	cattgtggta	cccctgggtg	480
tctcccggtg	tggaatccat	gaggaataca	atgaggagca	ctgtttttaa	tttcacaaag	540
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gccactcttt	actatcccac	caggagttct	gggctcagct	gaaaaaccta	ttttttatag	720
gggtcatcct	tgtttgtttc	cttccctacc	agttctttag	gatctattac	ttgaatgttg	780
tgacgcattc	caatgcctgt	aacagcaagg	ttgcatttta	taacgaaatc	ttcttgagtg	840
taacagcaat	tagctgctat	gatttgcttc	tctttgtctt	tgggggaagc	cattggttta	900
agcaaaagat	aattggctta	tggaattgtg	ttttgtgccg	ttagccacaa	actacagtat	960
tcataatttg	ttcctttata	ttgggaataa	aaatgggtat	aggggaggta	agaatggtat	1020
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agagccctca	ttgtagtcct	tatgggatcc	ctcccatctc	tgagtgatgg	ccgtacaaaag	1140
accagtgttg	ttgaatccac	ctggagttgc	aatattacat	tattttccag	tacagaatgt	1200
ctgtgtggcc	catgaaagca	acatagggtt	taagagtttt	agagtttcat	tagctcattc	1260
taagtctctc	tgtttgaagc	atggctctct	aggttttgga	ctgaactcag	acctttagtt	1320
cttttcatcc	cacttcacct	taggtaagta	aattctggcc	accaccagc	tccaaagaca	1380
caaactctcc	ttcgctaacc	aggttagatg	tccattcat	ctcatgccct	gataaaaact	1440
gataagggga	gagaatagtt	aaaaattttt	ctagggtatc	ataactctgg	taggaagtca	1500
tctgtctaga	aatcaagaga	aaaagaacgt	gtggcctcct	gttataacaa	gggtttctag	1560
atgtgtcctg	tgaaagggtg	tttaaggact	tggggatcaa	cttctcaat	tatcaccaat	1620
tgcactgttg	ctccaaaaat	cattttaaag	cttactggac	atatctacat	aatggtgaaa	1680
ctgtaattta	gagactatcc	ctgactaatg	tgctggtagg	cattaaaatg	agttcccaag	1740
ggaagtgatt	aaaatttttt	tctcttctgt	tttttgagag	aatttctaga	tgtcctgggc	1800
cacagttaat	taagattttt	aggggggaca	gaaagttata	ctgaaatctt	tagagctccc	1860

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ttccgccggtt aaaattatat atatatatat ttaaattata ccttaagttc tgggggtacat 1920
gtgcagaatg tgcaggtttg ttacataggt atacacgtgc catggtgggt tgcggcacct 1980
gtcaacccat ctacattagg tattttctct aatgctctcc ctcccctagc cccccacccc 2040
tggaacaggcc ccattgtgtg atgttcccct ccctgtgtcc atgtgttttc attgttcaac 2100
tcccacttct aagtgagaac atgcggtgtt tggttttctg ttctgtgtt agtttgctga 2160
gaatgatggt ttccaggta aaattatata tttttaaata aatgaaaact gtgtttttta 2220
aagaggactt ttgagaagta tatagaaaaa ccattaattt agactctgtg agattaggtt 2280
gcatgaagaa ggtttttctga atatttgaag agtggataaa taaatgtccc ccaaagcaat 2340
aaaatcataa tcctttaaaaa tataggaaaa ataactaatg ggaactaggc ttaataactg 2400
ggatgaaata atctgtacaa caaactccca tgacacatgt ttacctatgt aacaaacctg 2460
cacatgtacc cctgaactta aaataaaaatt taaagtataa taataaaata atatggattt 2520
tctttt 2525

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<210> 82
<211> 312
<212> PRT
<213> H.Sapiens

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<400> 82

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Met Thr Gly Asp Phe Pro Ser Met Pro Gly His Asn Thr Ser Arg Asn
1          5          10          15
Ser Ser Cys Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr Phe
          20          25          30
Ile Val Leu Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe Leu
          35          40          45
Leu Val Lys Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile Asn
          50          55          60
Leu Val Val Val His Ser Val Phe Leu Leu Thr Val Pro Phe Arg Leu
65          70          75          80
Thr Tyr Leu Ile Lys Lys Thr Trp Met Phe Gly Leu Pro Phe Cys Lys
          85          90          95
Phe Val Ser Ala Met Leu His Ile His Met Tyr Leu Thr Phe Leu Phe
          100          105          110
Tyr Val Val Ile Leu Val Thr Arg Tyr Leu Ile Phe Phe Lys Cys Lys
          115          120          125
Asp Lys Val Glu Phe Tyr Arg Lys Leu His Ala Val Ala Ala Ser Ala
130          135          140

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Gly Met Trp Thr Leu Val Ile Val Ile Val Val Pro Leu Val Val Ser
 145 150 155 160
 Arg Tyr Gly Ile His Glu Glu Tyr Asn Glu Glu His Cys Phe Lys Phe
 165 170 175
 His Lys Glu Leu Ala Tyr Thr Tyr Val Lys Ile Ile Asn Tyr Met Ile
 180 185 190
 Val Ile Phe Val Ile Ala Val Ala Val Ile Leu Leu Val Phe Gln Val
 195 200 205
 Phe Ile Ile Met Leu Met Val Gln Lys Leu Arg His Ser Leu Leu Ser
 210 215 220
 His Gln Glu Phe Trp Ala Gln Leu Lys Asn Leu Phe Phe Ile Gly Val
 225 230 235 240
 Ile Leu Val Cys Phe Leu Pro Tyr Gln Phe Phe Arg Ile Tyr Tyr Leu
 245 250 255
 Asn Val Val Thr His Ser Asn Ala Cys Asn Ser Lys Val Ala Phe Tyr
 260 265 270
 Asn Glu Ile Phe Leu Ser Val Thr Ala Ile Ser Cys Tyr Asp Leu Leu
 275 280 285
 Leu Phe Val Phe Gly Gly Ser His Trp Phe Lys Gln Lys Ile Ile Gly
 290 295 300
 Leu Trp Asn Cys Val Leu Cys Arg
 305 310

<210> 83
 <211> 1125
 <212> DNA
 <213> H.Sapiens

<400> 83
 gcaggagcac tgaaaatcag gaacaatcct gtattttttg tgataatcaa caaggacaaa 60
 acttctccat atgtaaaataa cagcggttatg agcagcaatt catccctgct ggtggctgtg 120
 cagctgtgct acgcgaacgt gaatgggtcc tgtgtgaaaa tccccttctc gccgggatcc 180
 cgggtgattc tgtacatagt gtttggtttt ggggctgtgc tggctgtgtt tggaacctc 240
 ctggtgatga tttcaatcct ccatttcaag cagctgcact ctccgaccaa ttttctcggt 300
 gcctctctgg cctgcgctga tttcttggtg ggtgtgactg tgatgccctt cagcatggtc 360
 aggacggtgg agagctgctg gtattttggg aggagttttt gtactttcca cacctgctgt 420
 gatgtggcat tttgttactc ttctctcttt cacttgctgt tcatctccat cgacaggtac 480
 attgcggtta ctgaccccct ggtctatcct accaagttca ccgtatctgt gtcaggaatt 540
 tgcacagcg tgtcctggat cctgcccctc atgtacagcg gtgctgtgtt ctacacaggt 600

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gtctatgacg atgggctgga ggaattatct gatgccctaa actgtatagg aggttgtcag      660
accgttgtaa atcaaaactg ggtgttgaca gattttctat ctttctttat acctaccttt      720
attatgataa ttctgtatgg taacatattt cttgtggcta gacgacaggc gaaaaagata      780
gaaaatactg gtagcaagac agaatcatcc tcagagagtt acaaagccag agtggccagg      840
agagagagaa aagcagctaa aaccctgggg gtcacagtgg tagcatttat gatttcatgg      900
ttaccatata gcattgattc attaattgat gcctttatgg gctttataac ccctgcctgt      960
atztatgaga tttgctgttg gtgtgcttat tataactcag ccatgaatcc tttgatttat     1020
gctttatttt acccatggtt taggaaagca ataaaagtta ttgtaactgg tcaggtttta     1080
aagaacagtt cagcaacat gaatttgttt tctgaacata tataa                        1125

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<210> 84
<211> 345
<212> PRT
<213> H.Sapiens

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<400> 84

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Met Ser Ser Asn Ser Ser Leu Leu Val Ala Val Gln Leu Cys Tyr Ala
1          5          10          15
Asn Val Asn Gly Ser Cys Val Lys Ile Pro Phe Ser Pro Gly Ser Arg
          20          25          30
Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala Val Leu Ala Val Phe
          35          40          45
Gly Asn Leu Leu Val Met Ile Ser Ile Leu His Phe Lys Gln Leu His
          50          55          60
Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala Cys Ala Asp Phe Leu
65          70          75          80
Val Gly Val Thr Val Met Pro Phe Ser Met Val Arg Thr Val Glu Ser
          85          90          95
Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe His Thr Cys Cys Asp
          100          105          110
Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu Cys Phe Ile Ser Ile
          115          120          125
Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val Tyr Pro Thr Lys Phe
          130          135          140
Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val Ser Trp Ile Leu Pro
145          150          155          160
Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly Val Tyr Asp Asp Gly
          165          170          175

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Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile Gly Gly Cys Gln Thr
 180 185 190
 Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe Leu Ser Phe Phe Ile
 195 200 205
 Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn Ile Phe Leu Val Ala
 210 215 220
 Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Gly Ser Lys Thr Glu Ser
 225 230 235 240
 Ser Ser Glu Ser Tyr Lys Ala Arg Val Ala Arg Arg Glu Arg Lys Ala
 245 250 255
 Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile Ser Trp Leu
 260 265 270
 Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly Phe Ile Thr
 275 280 285
 Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr Tyr Asn Ser
 290 295 300
 Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp Phe Arg Lys
 305 310 315 320
 Ala Ile Lys Val Ile Val Thr Gly Gln Val Leu Lys Asn Ser Ser Ala
 325 330 335
 Thr Met Asn Leu Phe Ser Glu His Ile
 340 345

<210> 85
 <211> 1020
 <212> DNA
 <213> H.Sapiens

<400> 85
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 tatggcatta tcttcctcgt gggatttcca ggcaatgcag tagtgatata cacttacatt 180
 ttcaaaatga gaccttggaa gagcagcacc atcattatgc tgaacctggc ctgcacagat 240
 ctgctgtatc tgaccagcct ccccttcctg attcactact atgccagtgg cgaaaactgg 300
 atctttggag atttcatgtg taagtttatc cgcttcagct tccatttcaa cctgtatagc 360
 agcatcctct tcctcacctg tttcagcatc ttccgctact gtgtgatcat tcaccaatg 420
 agctgctttt ccattcacia aactcgatgt gcagttgtag cctgtgctgt ggtgtggatc 480
 atttactggt tagctgtcat tccgatgacc ttcttgatca catcaaccaa caggaccaac 540
 agatcagcct gtctcgacct caccagttcg gatgaactca atactattaa gtggtacaac 600

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ctgattttga ctgcaagtac tttctgcctc cccttggtga tagtgacact ttgctataacc 660
acgattatcc acactttgac ccatggactg caaactgaca gctgccttaa gcagaaagca 720
cgaaggctaa ccattctgct actccttgca ttttacgtat gttttttacc cttccatatac 780
ttgaggggtca ttcaggatcg aatctcagcc tgctttcaat cagttgttcc attgagaatc 840
agatccatga agcttacatc gtttctagac cattatgctg ctctgaacac ctttggtaac 900
ctgttactat atgtgggtgt cagcgacaac tttcagcagg ctgtctgctc aacagtgaga 960
tgcaaagtaa gcgggaacct tgagcaagca aagaaaatta gttactcaaa caacccttga 1020

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<210> 86
 <211> 336
 <212> PRT
 <213> H.Sapiens

<400> 86

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Met Asn Glu Pro Leu Asp Tyr Leu Ala Asn Ala Ser Asp Phe Pro Asp
1          5          10          15
Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
          20          25          30
Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
          35          40          45
Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
          50          55          60
Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
65          70          75          80
Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
          85          90          95
Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
          100          105          110
Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
          115          120          125
Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
          130          135          140
His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
145          150          155          160
Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
          165          170          175
Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
          180          185          190

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Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Ser Thr Phe Cys
195 200 205

Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
210 215 220

Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
225 230 235 240

Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
245 250 255

Phe His Ile Leu Arg Val Ile Gln Asp Arg Ile Ser Ala Cys Phe Gln
260 265 270

Ser Val Val Pro Leu Arg Ile Arg Ser Met Lys Leu Thr Ser Phe Leu
275 280 285

Asp His Tyr Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val
290 295 300

Val Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys
305 310 315 320

Lys Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Ser Tyr Ser Asn
325 330 335

<210> 87

<211> 1138

<212> DNA

<213> H.Sapiens

<400> 87

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tgatttactc ttttattttt cctcctaggt ttctgggata agtatgtgca aataaaaaat      180
aaacatgaga aggaactgta acctgattat ggatttgga aaaagataaa tcaacacaca      240
aagggaaaag taaactgatt gacagccctc aggaatgatg cccttttgcc acaatataat      300
taatatttcc tgtgtgaaaa acaactggtc aaatgatgtc cgtgcttccc tgtacagttt      360
aatggtgctc ataattctga ccacactcgt tggcaatctg atagttattg tttctatatc      420
acacttcaaa caacttcata cccaacaaa ttggctcatt cattccatgg ccaactgtgga      480
ctttcttctg ggggtgctgg tcatgcctta cagtatgggt agatctgctg agcactgttg      540
gtattttggg gaagtcttct gtaaaattca cacaagcacc gacattatgc tgagctcagc      600
ctccattttc catttgtctt tcatctccat tgaccgctac tatgctgtgt gtgatccact      660
gagatataaa gccaagatga atatcttggt tatttgtgtg atgatcttca ttagttggag      720
tgtccctgct gtttttgcac ttggaatgat ctttctggag ctaaacttca aaggcgctga      780

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Val Tyr Tyr Arg Ile Tyr Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile
210 215 220

Ser Asp Ala Asn Gln Lys Leu Gln Ile Gly Leu Glu Met Lys Asn Gly
225 230 235 240

Ile Ser Gln Ser Lys Glu Arg Lys Ala Val Lys Thr Leu Gly Ile Val
245 250 255

Met Gly Val Phe Leu Ile Cys Trp Cys Pro Phe Phe Ile Cys Thr Val
260 265 270

Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Ala
275 280 285

Arg Gly Ser Arg Ala Asn Ser Ala
290 295

<210> 89

<211> 1023

<212> DNA

<213> H.Sapiens

<400> 89

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aatgatgtcc gtgcttcct gtacagtta atgggtgtca taattctgac cacactcgtt 120
ggcaatctga tagttattgt ttctatatca cacttcaaac aacttcatac cccaacaaat 180
tggctcattc attccatggc cactgtggac tttcttctgg ggtgtctggt catgccttac 240
agtatggtga gatctgctga gcaactgttg tattttggag aagtcttctg taaaattcac 300
acaagcaccg acattatgct gagctcagcc tccattttcc atttgtcttt catctccatt 360
gaccgctact atgctgtgtg tgatccactg agatataaag ccaagatgaa tatcttggtt 420
atgtgtgtga tgatcttcat tagttggagt gtcctgtctg tttttgcatt tggaatgatc 480
tttctggagc taaacttcaa aggcgctgaa gagatatatt acaaacatgt tcaactgcaga 540
ggaggttgct ctgtcttctt tagcaaaata tctgggggtac tgacctttat gacttctttt 600
tatatacctg gatctattat gttatgtgtc tattacagaa tatatcttat cgctaaagaa 660
caggcaagat taattagtga tgccaatcag aagctccaaa ttggattgga aatgaaaaat 720
ggaatttcac aaagcaaaga aaggaaagct gtgaagacat tggggattgt gatgggagtt 780
ttcctaatat gctggtgccc tttctttatc tgtacagtca tggacccttt tcttcaactac 840
attattccac ctactttgaa tgatgtattg atttggtttg gctacttgaa ctctacattt 900
aatccaatgg tttatgcatt tttctatcct tggtttagaa aagcactgaa gatgatgctg 960
tttggtaaaa ttttccaaaa agattcatcc aggtgtaaat tatttttgga attgagttca 1020
tag 1023

<210> 90
 <211> 339
 <212> PRT
 <213> H.Sapiens

<400> 90

Met	Met	Pro	Phe	Cys	His	Asn	Ile	Ile	Asn	Ile	Ser	Cys	Val	Lys	Asn
1				5					10					15	
Asn	Trp	Ser	Asn	Asp	Val	Arg	Ala	Ser	Leu	Tyr	Ser	Leu	Met	Val	Leu
			20					25					30		
Ile	Ile	Leu	Thr	Thr	Leu	Val	Gly	Asn	Leu	Ile	Val	Ile	Val	Ser	Ile
		35					40					45			
Ser	His	Phe	Lys	Gln	Leu	His	Thr	Pro	Thr	Asn	Trp	Leu	Ile	His	Ser
	50					55				60					
Met	Ala	Thr	Val	Asp	Phe	Leu	Leu	Gly	Cys	Leu	Val	Met	Pro	Tyr	Ser
65					70				75						80
Met	Val	Arg	Ser	Ala	Glu	His	Cys	Trp	Tyr	Phe	Gly	Glu	Val	Phe	Cys
				85					90					95	
Lys	Ile	His	Thr	Ser	Thr	Asp	Ile	Met	Leu	Ser	Ser	Ala	Ser	Ile	Phe
			100					105					110		
His	Leu	Ser	Phe	Ile	Ser	Ile	Asp	Arg	Tyr	Tyr	Ala	Val	Cys	Asp	Pro
	115						120					125			
Leu	Arg	Tyr	Lys	Ala	Lys	Met	Asn	Ile	Leu	Val	Ile	Cys	Val	Met	Ile
	130					135					140				
Phe	Ile	Ser	Trp	Ser	Val	Pro	Ala	Val	Phe	Ala	Phe	Gly	Met	Ile	Phe
145					150				155						160
Leu	Glu	Leu	Asn	Phe	Lys	Gly	Ala	Glu	Glu	Ile	Tyr	Tyr	Lys	His	Val
				165					170					175	
His	Cys	Arg	Gly	Gly	Cys	Ser	Val	Phe	Phe	Ser	Lys	Ile	Ser	Gly	Val
			180					185					190		
Leu	Thr	Phe	Met	Thr	Ser	Phe	Tyr	Ile	Pro	Gly	Ser	Ile	Met	Leu	Cys
		195					200					205			
Val	Tyr	Tyr	Arg	Ile	Tyr	Leu	Ile	Ala	Lys	Glu	Gln	Ala	Arg	Leu	Ile
	210					215					220				
Ser	Asp	Ala	Asn	Gln	Lys	Leu	Gln	Ile	Gly	Leu	Glu	Met	Lys	Asn	Gly
225					230					235					240
Ile	Ser	Gln	Ser	Lys	Glu	Arg	Lys	Ala	Val	Lys	Thr	Leu	Gly	Ile	Val
				245					250					255	
Met	Gly	Val	Phe	Leu	Ile	Cys	Trp	Cys	Pro	Phe	Phe	Ile	Cys	Thr	Val
			260					265					270		

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Met Asp Pro Phe Leu His Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val
 275 280 285

Leu Ile Trp Phe Gly Tyr Leu Asn Ser Thr Phe Asn Pro Met Val Tyr
 290 295 300

Ala Phe Phe Tyr Pro Trp Phe Arg Lys Ala Leu Lys Met Met Leu Phe
 305 310 315 320

Gly Lys Ile Phe Gln Lys Asp Ser Ser Arg Cys Lys Leu Phe Leu Glu
 325 330 335

Leu Ser Ser

<210> 91
 <211> 1696
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 <213> H.Sapiens

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 cacagcaccg tctctcccat actcggatcat tcacaccatc attgattcac caggcaccac 180
 tccgtgtcca gcaggactct ggggacccca aatggacact accatggaag ctgacctggg 240
 tgccactggc cacaggcccc gcacagagct tgatgatgag gactcctacc cccaaggatg 300
 ctgggacacg gtcttcctgg tggccctgct gctccttggg ctgccagcca atgggttgat 360
 ggcgtggctg gccggctccc aggcccgga tggagctggc acgcgtctgg cgctgctcct 420
 gctcagcctg gccctctctg acttcttgtt cctggcagca gcggccttcc agatcctaga 480
 gatccggcat gggggacact ggccgctggg gacagctgcc tgccgcttct actacttct 540
 atggggcgtg tctactcct ccggcctctt cctgctggcc gccctcagcc tcgaccgctg 600
 cctgctggcg ctgtgcccac actggtaccc tgggcaccgc ccagtccgcc tgcccctctg 660
 ggtctgcgcc ggtgtctggg tgctggccac actcttcagc gtgccctggc tgggtcttccc 720
 cgaggctgcc gtctggtggt acgacctggt catctgcctg gacttctggg acagcgagga 780
 gctgtcgtg aggatgctgg aggtcctggg gggcttctct ccttctctcc tgctgctcgt 840
 ctgccacgtg ctcacccagg ccacagcctg tcgcacctgc caccgccaac agcagcccg 900
 agcctgccgg ggcttcgccc gtgtggccag gaccattctg tcagcctatg tggtcctgag 960
 gctgccctac cagctggccc agctgctcta cctggccttc ctgtgggacg tctactctgg 1020
 ctacctgtc tgggaggccc tgggtctact cgactacctg atcctactca acagctgcct 1080
 cagccccttc ctctgcctca tggccagtgc cgacctccgg accctgctgc gctccgtgct 1140

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ctcgtccttc gcggcagctc tctgcgagga gcggccgggc agcttcacgc ccaactgagcc 1200
acagacccag ctagattctg agggccaac tctgccagag ccgatggcag agggccagtc 1260
acagatggat cctgtggccc agcctcaggt gaaccccaca ctccagccac gatcggatcc 1320
cacagctcag ccacagctga accctacggc ccagccacag tcggatcca cagcccagcc 1380
acagctgaac ctcatggccc agccacagtc agattctgtg gcccagccac aggcagacac 1440
taacgtccag acccctgcac ctgctgccag ttctgtgccc agtcctgtg atgaagcttc 1500
cccaacccca tctctgcac ctaccccagg ggccttgag gaccagcca cacctcctgc 1560
ctctgaagga gaaagcccca gcagacccc gccagaggcg gcccgggcg caggccccac 1620
gtgagggtcc aggaacacgc agggccacca gagcagtga agagcccagg gcagacagag 1680
gaaccagcca gtcaga 1696

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<210> 92
<211> 505
<212> PRT
<213> H.Sapiens

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<400> 92

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Leu Ala Trp Arg Cys Thr Ala Pro Ser Leu Pro Tyr Ser Val Ile His
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20          25          30
Gly Pro Gln Met Asp Thr Thr Met Glu Ala Asp Leu Gly Ala Thr Gly
35          40          45
His Arg Pro Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly
50          55          60
Gly Trp Asp Thr Val Phe Leu Val Ala Leu Leu Leu Leu Gly Leu Pro
65          70          75          80
Ala Asn Gly Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly
85          90          95
Ala Gly Thr Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp
100         105         110
Phe Leu Phe Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His
115         120         125
Gly Gly His Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe
130         135         140
Leu Trp Gly Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu
145         150         155         160

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Ser Leu Asp Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly
 165 170 175
 His Arg Pro Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val
 180 185 190
 Leu Ala Thr Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala
 195 200 205
 Val Trp Trp Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu
 210 215 220
 Glu Leu Ser Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe
 225 230 235 240
 Leu Leu Leu Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg
 245 250 255
 Thr Cys His Arg Gln Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg
 260 265 270
 Val Ala Arg Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr
 275 280 285
 Gln Leu Ala Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser
 290 295 300
 Gly Tyr Leu Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu
 305 310 315 320
 Leu Asn Ser Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp
 325 330 335
 Leu Arg Thr Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu
 340 345 350
 Cys Glu Glu Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln
 355 360 365
 Leu Asp Ser Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln
 370 375 380
 Ser Gln Met Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln
 385 390 395 400
 Pro Arg Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln
 405 410 415
 Pro Gln Ser Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln
 420 425 430
 Pro Gln Ser Asp Ser Val Ala Gln Pro Gln Ala Asp Thr Asn Val Gln
 435 440 445
 Thr Pro Ala Pro Ala Ala Ser Ser Val Pro Ser Pro Cys Asp Glu Ala
 450 455 460
 Ser Pro Thr Pro Ser Ser His Pro Thr Pro Gly Ala Leu Glu Asp Pro
 465 470 475 480

ccagaggcg ccccgggcgc agggccacg tga

1413

<210> 94
 <211> 419
 <212> PRT
 <213> H.Sapiens

<400> 94

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Arg Thr Glu Leu Asp Asp Glu Asp Ser Tyr Pro Gln Gly Gly Trp Asp
 20 25 30

Thr Val Phe Leu Val Ala Leu Leu Leu Gly Leu Pro Ala Asn Gly
 35 40 45

Leu Met Ala Trp Leu Ala Gly Ser Gln Ala Arg His Gly Ala Gly Thr
 50 55 60

Arg Leu Ala Leu Leu Leu Leu Ser Leu Ala Leu Ser Asp Phe Leu Phe
 65 70 75 80

Leu Ala Ala Ala Ala Phe Gln Ile Leu Glu Ile Arg His Gly Gly His
 85 90 95

Trp Pro Leu Gly Thr Ala Ala Cys Arg Phe Tyr Tyr Phe Leu Trp Gly
 100 105 110

Val Ser Tyr Ser Ser Gly Leu Phe Leu Leu Ala Ala Leu Ser Leu Asp
 115 120 125

Arg Cys Leu Leu Ala Leu Cys Pro His Trp Tyr Pro Gly His Arg Pro
 130 135 140

Val Arg Leu Pro Leu Trp Val Cys Ala Gly Val Trp Val Leu Ala Thr
 145 150 155 160

Leu Phe Ser Val Pro Trp Leu Val Phe Pro Glu Ala Ala Val Trp Trp
 165 170 175

Tyr Asp Leu Val Ile Cys Leu Asp Phe Trp Asp Ser Glu Glu Leu Ser
 180 185 190

Leu Arg Met Leu Glu Val Leu Gly Gly Phe Leu Pro Phe Leu Leu Leu
 195 200 205

Leu Val Cys His Val Leu Thr Gln Ala Thr Ala Cys Arg Thr Cys His
 210 215 220

Arg Gln Gln Gln Pro Ala Ala Cys Arg Gly Phe Ala Arg Val Ala Arg
 225 230 235 240

Thr Ile Leu Ser Ala Tyr Val Val Leu Arg Leu Pro Tyr Gln Leu Ala
 245 250 255

Gln Leu Leu Tyr Leu Ala Phe Leu Trp Asp Val Tyr Ser Gly Tyr Leu

260

265

270

Leu Trp Glu Ala Leu Val Tyr Ser Asp Tyr Leu Ile Leu Leu Asn Ser
 275 280 285
 Cys Leu Ser Pro Phe Leu Cys Leu Met Ala Ser Ala Asp Leu Arg Thr
 290 295 300
 Leu Leu Arg Ser Val Leu Ser Ser Phe Ala Ala Ala Leu Cys Glu Glu
 305 310 315 320
 Arg Pro Gly Ser Phe Thr Pro Thr Glu Pro Gln Thr Gln Leu Asp Ser
 325 330 335
 Glu Gly Pro Thr Leu Pro Glu Pro Met Ala Glu Ala Gln Ser Gln Met
 340 345 350
 Asp Pro Val Ala Gln Pro Gln Val Asn Pro Thr Leu Gln Pro Arg Ser
 355 360 365
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Pro Thr Ala Gln Pro Gln Ser
 370 375 380
 Asp Pro Thr Ala Gln Pro Gln Leu Asn Leu Met Ala Gln Pro Gln Ser
 385 390 395 400
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 405 410 415

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<210> 95
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49

<210> 96
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<400> 96
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49

<210> 97
 <211> 22
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<400> 97
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<210> 98
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<400> 98
 aaacttctct gcccttaccg tc 22

<210> 99
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<400> 99
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<210> 100
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<400> 100
 catgatcaac ctgagcgtca c 21

<210> 101
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<400> 101
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28

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<400> 102
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30

<210> 103
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<210> 104
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<400> 104
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19

<210> 106
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18

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33

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<400> 108
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33

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<400> 111
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<210> 115
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34

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<400> 116
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<400> 117
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<210> 118
 <211> 22
 <212> DNA
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<400> 118
 ccgcaggagc aatgaaaatc ag 22

<210> 119
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<400> 119
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<210> 120
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<400> 120
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<210> 121
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<400> 121
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<210> 122
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22

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22

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<210> 133
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<210> 134
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<400> 134
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<210> 135
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<400> 136
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<400> 137
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23

<210> 138
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<220>
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<400> 138
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49

<210> 139
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<210> 140
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21

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<210> 144
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<210> 146
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<210> 148
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<220>
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<400> 148
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29

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<220>
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<400> 155
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<210> 156
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<220>
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49

<210> 157
 <211> 35
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<220>
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35

<210> 158
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<220>
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31

<210> 159
 <211> 52
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<220>
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52

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 <212> DNA
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<220>
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<400> 160
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<210> 161
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48

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 <211> 24
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<213> Artificial Sequence

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<400> 162

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24

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<212> DNA

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<400> 164

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24

<210> 165

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<212> DNA

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<223> Novel Sequence

<400> 165

gcgtaatagc actcactata gggagaccgc acaaaacaca attccataag cc

52

<210> 166

<211> 23

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<220>

<221> misc_feature
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<400> 166
 gctacgccac tctttactat ccc

23

<210> 167
 <211> 49
 <212> DNA
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<400> 167
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49

<210> 168
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<400> 168
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20

<210> 169
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<400> 169
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48

<210> 170
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<400> 170
ttatgagcag caattcatcc c 21

<210> 171
<211> 49
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<400> 171
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<210> 172
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<212> DNA
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<400> 172
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<210> 173
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<400> 173
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<400> 174
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<210> 175
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<400> 175
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<210> 176
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<400> 176
 agaagacaga gcaacctcc 19

<210> 177
 <211> 47
 <212> DNA
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<400> 177
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<210> 178
 <211> 22
 <212> DNA
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<220>
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<400> 178
 ctgtaaaatt cacacaagca cc 22

<210> 179

<211> 31
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<220>
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<400> 179
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31

<210> 180
 <211> 31
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<400> 180
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31

<210> 181
 <211> 20
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<400> 181
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<210> 182
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<220>
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<400> 182
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22

<210> 183
 <211> 20
 <212> DNA
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<220>
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<400> 183
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<210> 184
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 184
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<210> 185
 <211> 1188
 <212> DNA
 <213> H.Sapiens

<400> 185
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 atgggccccg gcgaggcgct gctggcgggg ctcttggtga tggtagctggc cgtggcgctg 120
 ctatccaacg cactggtgct gctttgttgc gcctacagcg ctgagctccg cactcgagcc 180
 tcaggcgctc tcttggtgaa tctgtctctg ggccacctgc tgetggcggc gctggacatg 240
 cccttcacgc tgctcggtgt gatgcgcggg cggacaccgt cggcgcccgg cgcattgcca 300
 gtcattggct tcttggaac cttcttggcg tccaacgcgg cgtgagcgt ggcggcgctg 360
 agcgagacc agtggctggc agtgggcttc cactgcgct acgcccggacg cctgcgaccg 420
 cgctatgccg gctgctgct gggctgtgcc tggggacagt cgtggcctt ctcaggcgct 480
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 agacactgcc agcgcatgga caccgtcacc atgaaggcgc tcgctgctgct cgccgacctg 720
 caccacagtg tgcggcagcg ctgcctcatc cagcagaagc ggccgcca ccgcgccacc 780
 aggaagattg gcattgctat tgcgacctc ctcactgtgct ttgccccgta tgtcatgacc 840
 aggctggcgg agctcgtgcc cttcgtcacc gtgaacgccc agtggggcat cctcagcaag 900

tgcctgacct acagcaaggc ggtggccgac ccgttcacgt actctctgct ccgccggccg 960
 ttccgccaag tcctggcccg catggtgcac cggctgctga agagaacccc gcgccagca 1020
 tccacccatg acagctctct ggatgtggcc ggcatggtgc accagctgct gaagagaacc 1080
 ccgcgcccag cgtccaccca caacggctct gtggacacag agaatgattc ctgcctgcag 1140
 cagacacact gagggcctgg cagggctcat cgtcccccacc ttctaaga 1188

<210> 186
 <211> 363
 <212> PRT
 <213> H.Sapiens

<400> 186

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 Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys Ala Tyr
 20 25 30
 Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
 35 40 45
 Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
 50 55 60
 Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
 65 70 75 80
 Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser
 85 90 95
 Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu
 100 105 110
 Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly
 115 120 125
 Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
 130 135 140
 Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
 145 150 155 160
 Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu
 165 170 175
 His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
 180 185 190
 Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met Asp Thr
 195 200 205
 Val Thr Met Lys Ala Leu Ala Leu Leu Ala Asp Leu His Pro Ser Val

210

215

220

Arg Gln Arg Cys Leu Ile Gln Gln Lys Arg Arg Arg His Arg Ala Thr
 225 230 235 240

Arg Lys Ile Gly Ile Ala Ile Ala Thr Phe Leu Ile Cys Phe Ala Pro
 245 250 255

Tyr Val Met Thr Arg Leu Ala Glu Leu Val Pro Phe Val Thr Val Asn
 260 265 270

Ala Gln Trp Gly Ile Leu Ser Lys Cys Leu Thr Tyr Ser Lys Ala Val
 275 280 285

Ala Asp Pro Phe Thr Tyr Ser Leu Leu Arg Arg Pro Phe Arg Gln Val
 290 295 300

Leu Ala Gly Met Val His Arg Leu Leu Lys Arg Thr Pro Arg Pro Ala
 305 310 315 320

Ser Thr His Asp Ser Ser Leu Asp Val Ala Gly Met Val His Gln Leu
 325 330 335

Leu Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asn Gly Ser Val Asp
 340 345 350

Thr Glu Asn Asp Ser Cys Leu Gln Gln Thr His
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<210> 187
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
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<400> 187
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29

<210> 188
 <211> 28
 <212> DNA
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<220>
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<400> 188
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28

<210> 189
 <211> 20

<212> DNA
<213> Artificial Sequence

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<221> misc_feature
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<400> 189
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<210> 190
<211> 18
<212> DNA
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<400> 190
ttggacgccca ggaaggtg

18